Appl

Sequence 6, 1 Sequence 39,

Sequence

Sequence 6, Appli Sequence 2, Appli Sequence 6, Appli

Sequence 15, Sequence 15, Sequence 4,

Sequence Sequence Appl Appli Appli

Sequence 2, 7 Sequence 23,

Sequence 6, Sequence

Sequence 1, Application 10, Application 10, Application 1, Applica

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RESULT 1
US-08-347-492B-11
Sequence 11, Application US/08347492B
Fatent No. 5602008
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOXINES, THEIR
TITLE OF INVENTION: EXPRESSED CHEMOXINES, THEIR
TITLE OF INVENTION: EXPRESSED CHEMOXINES, CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSS:
CORRESPONDENCE ADDRESSS:
US-08-330-163-15

US-08-482-111-15

US-08-479-126B-6

US-08-726-830A-6

US-08-726-830A-6

US-09-044-856A-6

US-09-044-856A-6

US-09-044-856A-6

US-09-044-856A-6

US-09-121-450-2

US-09-121-450-2

US-09-121-450-2

US-09-121-450-2

US-09-121-450-2

US-09-121-450-2

US-09-121-450-2

US-09-121-450-2

US-08-177-36B-1

US-08-177-36B-1

US-08-177-36B-1

US-08-177-346A-3

US-08-177-346A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/347,492B
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-CCT-1994
ATTORNEY/AGENT INFORMATION:
NAMM: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: 9F-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: GENBANK
CLONE: GI 127080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-347-492B-11
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  Sequence 11, Appl
Sequence 4, Appli
Sequence 11, Appl
Sequence 11, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 6, Appli
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                                                                                       December 16, 2003, 15:36:20 ; Search time 14.5792 Seconds (without alignments) 266.996 Million cell updates/sec
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Sequence 159,
                                                                                                                                                                     1 MKLCVTVLSLLMLVAAFCSP.......VCADPSBSWVQEYVYDLELN 92
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Sequence
Sequence
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Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*
1: /cgn2_6/ptodate1/liaa/SA_COMB.pep:*
2: /cgn2_6/ptodate1/liaa/SB_COMB.pep:*
3: /cgn2_6/ptodate1/liaa/6A_COMB.pep:*
4: /cgn2_6/ptodate1/liaa/6B_COMB.pep:*
5: /cgn2_6/ptodate1/liaa/PCTUG_COMB.pep:*
6: /cgn2_6/ptodate1/liaa/PCTUG_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-679-493A-157
US-09-679-493A-158
US-09-230-371A-24
US-09-230-637-41
US-08-679-493A-159
US-07-792-988-2
US-07-792-988-2
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US-08-679-493A-160
US-08-480-449-22
                                                                                                                                                                                                                                                        al number of hits satisfying chosen parameters:
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US-08-375-346A-4
US-08-421-144A-4
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US-07-982-759F-35
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US-08-467-123B-4
US-08-808-720-10
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US-08-479-603-22
US-08-939-107-22
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JS-08-716-188-6
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein - protein search, using sw model
                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
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Match Length DB
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYBTSSLCSQ 60
                                                                                  1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                        0; Gaps
                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Coleman, Roger
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,
TITLE OF INVENTION: ITS PRODUCTION AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 486; DB 1; Length 92; Best Local Similarity 100.0%; Pred. No. 1.3e-50; Matches 92; Conservative 0; Mismatches 0; Indels
Query Match 100.0%; Score 486; DB 1; Length 92; Sest Local Similarity 100.0%; Pred. No. 1.3e-50; Atches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                       61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                          61 PAVVFOTKRSKOVCADPSESWVOEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0026 US
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19-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/27-CTANCORD
                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08375346A
Patent No. 5605817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: LUTHER, BARBARA J. 954
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 855-0555
TELEFAX: (415) 855-0572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: COLEMAN ROGER
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 486; DB 2; Length 92; Best Local Similarity 100.0%; Pred. No. 1.3e-50; Matches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144A
FILING DATE: 13-APR.1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08798143

Patent No. 5936068

GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Sailhamer, Jeffrey J.
ITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
ITLE OF INVENTION: PRODUCTION AND USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                         US-08-421-144A-4; Sequence 4, Application US/08421144A; Patent No. 5874211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELBERAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 486; DB 2; Length 92; 100.0%; Pred. No. 1.3e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Coleman, Roger
APPLICANT: Wilde, Craig C
APPLICANT: Wilde, Craig C
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STREET: CA
STATE: CA
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ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                              CURRENT APPLICATION DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,143
FILING DATE: 10-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
APPLICATION: 536
                                                                                                                                                                                                               FILING DATE: 10-FEB-1997
CLASSIFTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,492
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/30,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0024
                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08467123B Atent No. 5945506
GENERAL INFORMATION:
                                                                                                                 E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity 100. Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YPE: amino acid
TRANDEDNESS: single
                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
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CLONE: GI 127080
-08-798-143-11
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       STREET: 31/7
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-08-467-123B-4
                                                                  COUNTRY:
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1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08808720
Fatent No. 6100397
GENERAL INPORMATION:
APPLICANT: Swanberg, Stephen
TITLE OF INVENTION: CHIMERIC POLYBEPTIDES CONTAINING
TITLE OF INVENTION: CHEMOKINE DOMAINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 486; DB 2; Local Similarity 100.0%; Pred. No. 1.3e-50; Les 92; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,123B
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-555-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Genetics Insititute, Inc
87 CambridgePark
                                                                                                                                         FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,346
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: GI5291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 92 amino acids TYPE: amino acid
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REGISTRATION NUMBER: p-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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CLASSIFICATION:
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ZIP: 02140
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Query Match
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APPLICANT: Fife, Kenneth H.
APPLICANT: Krathwohl, Mitchell D.
APPLICANT: Krathwohl, Mitchell D.
APPLICANT: Hromas, Robert
APPLICANT: Broxmeyer, Hal E.
TITLE OF INVENTION: FUNCTIONAL CHARACTERIZATION OF THE C-C CHEMOKINE-LIKE
TITLE OF INVENTION: MOLECULES ENODED BY MOLLUSCUM CONTAGIOSUM VIRUS TYPES I
TITLE OF INVENTION: MOLECULES ENODED BY MOLLUSCUM CONTAGIOSUM VIRUS TYPES I
TITLE OF INVENTION: MOLECULES ENODED BY MOLLUSCUM CONTAGIOSUM VIRUS TYPES I
CURRENT APPLICATION NUMBER: US/09/133,521
CURRENT APPLICATION NUMBER: 60/055,532
EARLIER FILING DATE: 1994-08-15
BARLIER FILING DATE: 1997-08-15
SOFTWARE: PATENTIN VOS: 30
SOFTWARE: PATENTIN VOS: 30
                                                                                                                                                                                                                                                                                                                                            1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
TILLE BEFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR PILING DATE: 1995-07-14
                                                                                                                                                                                                                                   100.0%; Score 486; DB 3; Length 92; 100.0%; Pred. No. 1.3e-50; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09133521
Patent No. 6281200
GENERAL INFORMATION:
                                                LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 92; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         92; Conservative
                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
3-08-808-720-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                             Best Local Similarity
Matches 92; Conserv
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3-08-679-493A-157
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3-09-133-521-6
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APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Rose, James J
APPLICANT: Moore, Datick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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Patent No. 6303295

GENERAL INFORMATION:
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS

TITLE OF INVENTION NUMBER: US/08/679,493A

CURRENT FILING DATE: 1996-07-12

PRIOR APPLICATION NUMBER: 60/001203

PRIOR APPLICATION NUMBER: 60/001203

PRIOR PILING DATE: 1995-07-14

PRIOR PILING DATE: 1995-09-01

NUMBER OF SEQ ID NOS: 216

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 486; DB 4; Length 92; 100.0%; Pred. No. 1.3e-50; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             100.0%; Score 486; DB 4; Length 92; 100.0%; Pred. No. 1.3e-50; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 24, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                     SEQ ID NO 157
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                                                                                                                                 LENGTH: 92
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61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
            61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                      ; GENERAL INFORMATION:
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                                                                                                                            US-09-230-637-41
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Herrmann, Steve
APPLICANT: Wanberg, Stephen
TITLE OF INVENTION: CHIMBRIC POLYPEPTIDES CONTAINING
TITLE OF INVENTION: CHEMOKINE DOMAINS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,720
                                                                                                                                                                                                                                                                                                                                                                                    61 PAVVFOTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                   61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Genetics Insititute, Inc.
87 CambridgePark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08808720 Patent No. 6100387
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REGISTRATION NUMBER: P-41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GI:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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amino acid
                                                                                                                                                                                                                                   92; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02140
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STREET: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-08-808-720-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-808-720-7
                                                                                                                                                                                          Query Match
Best Local S
Matches 92
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1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                        APPLICANT: Nicholas, John
APPLICANT: Nicholas, John
APPLICANT: Nicholas, John
APPLICANT: Nicholas, John
APPLICANT: Reatz, Marvin
TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
TITLE OF INVENTION: 1007.8837
CURRENT APPLICATION NUMBER: US/09/230,637
PRIOR APPLICATION NUMBER: 60/022.591
PRIOR FILING DATE: 1996-07-25
PRIOR FILING DATE: 1996-07-25
PRIOR FILING DATE: 1997-07-44
NUMBER OF SEQ ID NOS: 62
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TAYLOR, Ethan W.

TILLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS FILE REPERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ 12 NOS: 216
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.2%; Score 482; DB 3; Length 92; 98.9%; Pred. No. 3.9e-50; tive 0; Mismatches 1; Indels
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; Sequence 41, Application US/09230637; Patent No. 6264958
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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APPLICANT: Gewirtz, Alan M.
TITLE OF INVENTION: Suppression of megakaryo-
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.9%; Score 476; DB 1; Length 92; Best Local Similarity 98.9%; Pred. No. 2e-49; Matches 91; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.2.1.6
ZIP: 19104-3246
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/792,988
TYLING DATE: 19911115
                             61 PAVVFQTKRGKQVCADPSESWVQEYVYDLELN 92
61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                     University of Pennsylvania
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Patent No. 6548654
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6656-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5349
TELEX: No. 5306709-
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           Sequence 2, Application US/07792988
Patent No. 5306709
                                                                                                                                                                                                                                                                                                                                       STREET: Suite 419
STREET: 133 South 36th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single stranded
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Bacon, Kevin B.
Bazan, J. Fernando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                              CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
STRANDEDNESS: sir
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3-07-792-988-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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1 MKLCVSALSLILLVAAFCAPGFSAPMGSDPPTSCCFSYTARKLPRNFVVDYYETSSLCSQ 60
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APPLICANT: Schall, Thomas J.

PEPLICANT: Zlotnik, Albert
TILLE OF INVENTION: Mammalian CX3C Chemokine Genes
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CARRESED: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Felease #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,006A FILING DATE: 16-MAY-1996
CLASSIFICATION: 536
CLASSIFICATION: 536
FILING DATE: A-JAN-1996
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: December 16, 2003, 15:40:17 Job time : 14.5792 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0569K
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 92.4?
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

:uo r

December 16, 2003, 15:36:20 ; Search time 13.4262 Seconds

(without alignments) 651.810 Million cell updates/sec

US-09-920-137A-8

1 MKVSAARLAVILIATALCAP......VCANPEKKWVREYINSLEMS 91 ile: rfect score: inence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** oring table:

al number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

arched:

%t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries iimum DB seq length: 0
iimum DB seq length: 200000000

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*

abase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Nyalternate names: Murantes Cybecies: Mus musculus (house mouse) Cybecies: Nus musculus (house mouse) Cybecession: 148875; A46539; T48654; 156970 Cyaccession: 148875; A46539; T48664; 156970 Cyaccession: 152, 1182-1189, 1994 Arritle: Cloning, genomic organization, and chromosomal localization of the Scya5 gene Arritle: Cloning, genomic organization, and chromosomal localization of the Scya5 gene Ayaccession: 148875 Ayaccession: 148875 Ayaccession: 148875 Ayaccession: 148875

monocyte chemoattractant cytokine RANTES precursor - mouse

interleukin-8 prec cytokine SDF-1.bet interleukin-8 - do Neutrophil attract interleukin-8 prec pre-B-cell growth- interleukin-8 homo cytokine - mouse I-309 protein prec lymphotactin precu interleukin-8 - ra monocyte chemotact	RSV-induced protei	hypothetical_prote
542496 G01540 JW0841 A53096 A53096 A53497 153416 181182 ETMSL A56871 A56871 A26736	150417	T22187
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106.5 106.5 103 103 103 99 99 96.5 95 95	69	99
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ALIGNMENTS

RESULT 1 A28815	
 Monocyte chemoattractant cytokine RANTES precursor - human Nyllternate names: small inducible cytokine A5; T-cell specific cytokine RANTES C:Specifes: Homo canions (man)	
 C;Date: 30-Jun-1989 #sequence_revision 16-Aug-1996 #text_change 29-May-1998 C;Accession: A28815	
 vis, M.M.;	×
A, Title: A human T cell-specific molecule is a member of a new gene family. A, Reference number: A28815; MUID:88285659; PMID:2456327	
A;Accession: A28815 A;Molecule type: mRNA A;Resdines: 1-91.9000	
A;Cross-references: GB:M21121 C;Comment: The acronym RANTES reflects the description "Reculated upon Acrivation Norm	E
 C;Genetics; A:Gene: GDB:SCVAS: n1201369	:
 A;Cross-references: GDB:120749; OMIM:187011 A:Map position: 1771 2-1771	
C;Superfamily: macrophage inflammatory protein C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell	
 F:1-23/Domain: signal sequence #status predicted <sig> F:24-91/Product: T-cell protein RANTES #status predicted <mat></mat></sig>	
 Query Match Best Local Similarity 98.9%; Pred. No. 2.4e-44; Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
 QY 1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60	
 Db 1 MKVSAAALAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60	
REY	
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91	

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A; Molecule type: DNA
A; Mesidues: 1-93 «NAK.
A; Residues: 1-93 «NAK.
A; Residues: 1-93 «NAK.
A; Residues: 1-93 «NAK.
A; Residues: 1-93 «NAK.
A; Cross = reference: GB.
Cross = reference in GB.
Cro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LD78-beta protein precursor - human

NyAlternate names: macrophage inflammatory protein homolog GOS19-2; small inducible cyt.

Syspeciaes: Homo sapiens (man)

C,Dete: 28-Sep-1990 #sequence revision 28-Sep-1990 #text_change 20-Jun-2000

C,Accession: B35673; B30412; $10157; B30908

My Noahyama, H.; Shimada, K.

Mol. Cell. Biol. 10, 3646-3658, 1990

A;Title: Structures of human genes coding for cytokine LD78 and their expression.

A;Reference number: A35673; MUID:90287155; PMID:1694014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:X52149; NID:g34750; PIDN:CAA36397.1; PID:g296666
Comment: This protein is a member of a "small inducible" or "activation specific" gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 macrophage inflammatory protein 1-alpha precursor - human N_1 Alternate names: LD78-alpha protein precursor; lymphocyte tumor promoter-induced prot
                     1 MKVSAARLAVILIATALCAPASASPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MQVSTAALAVLLCTMALCNQVLSAPLAADTPTACCFSYTSRQIPQNFIADYFETSSQCSK 60
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C;Species: Homo sapiens (man)
C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ajintrons: 26/1; -64/2
S.Superfamily: macrophage inflammatory protein
C;Keywords: cytokine
P;1-22/Domain: signal sequence #status predicted <SIG>
F;23-93/Product: LD78-beta protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.8%; Score 252.5; DB 247.8%; Pred. No. 1.9e-20;
                                                                                                                                                                            60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                        61 PAVVFOTKKGROVCANPSESWVOEXVDDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GDB:120369; OMIM:182284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Conservative
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Residues: 1-93 <IRV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
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A; Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB:SCYA4
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Residues: 1-18, 74, 20-91 < SCH
Residues: 1-18, 74, 20-91 < SCH
Residues: 1-18, 70-91 < S
Residues: 1-91 <DAN>
Zross-references: EMBL:U02298; NID:g460090; PIDN:AAA18302.1; PID:g460091
Schall, T.O.; Simpson, N.O.; Mak, J.Y.
c. J. Immunol. 22, 1477-1481, 1992
Fitle: Molecular cloning and expression of the murine RANTES cytokine: structural and Reference number: A46539; MUID:92289805; PMID:1376260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocession: 146730 Compared to the control of the course of acute in efference number: 146730; MULTARAMI, K.; Ohkawara, S.; Yoshinaga, M. Immunol. 6, 149-156, 1994 in mRNA expression of neutrophils during the course of acute in eference number: 146730; MUID:94198229; PMID:8148323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tesidues: 1.40, 'E',42-91 <NEI>
Toss-references: GB:M7747; NID:g200649; PIDN:AAA40029.1; PID:g200650
Jomment: This chemoattractant for monocytes but not neutrophils is an immediate-early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tross-references: EMBL:X70675; NID:g475205; PIDN:CAA50011.1; PID:g475206
Tellson, B.G.; Krensky, A.
Haby Int. 41, 220-225, 1992
Ritle: Isolation and characterization of cDNA from renal tubular epithelium encoding
Reference number: I56970; MUID:92277990; PMID:1375672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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'pecies: Oryctolagus cuniculus (domestic rabbit)

'ate: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       !uperfamily: macrophage inflammatory protein
(eywords: chemotaxis; cytokine; immediate-early protein; inflammation
-23/Domain: signal sequence #status predicted <SIG>
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51.1%; Pred. No. 1.2e-20;
iive 16; Mismatches 28;
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desidues: 1-91 <SHI>
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esidues: 1-92 <MOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: I48654
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1; Gaps

DB 2; Length 93; Indels

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60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                         Best Local Similarity
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A; Residues: 1-92 < DAU>
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A, Residues: 1-92 <SHE>
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                                                                  Matches
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Blum, S.; Forsdyke, R.E.; Forsdyke, D.R.
A Cell Biol. 9, 589-602, 1990
Title: Three human homologs of a murine gene encoding an inhibitor of stem cell prolif
Reference number: A30412; MJID:91103879; PMID:2271120
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5hi, M. J. Godleski, J.J.; Paulauskis, J.D.
ochem. Biophys. Res. Commun. 211, 289-295, 1995
Fitle: Molecular cloning and posttranscriptional regulation of macrophage inflammatory
Reference number: 152322; MUID:95298037; PMID:7779098
                                                                                                                                                                               Molecule type: DNA
Residues: 1.92 ×NAX.
Cross references: GB:D90144; NID:g219905; PIDN:BAA14172.1; PID:g219906
Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.
Immunol: 142, 1582-1590, 1989
Title: Mitogenic activation of human T cells induces two closely related genes which
Reference number: A30574; MUID:89140347; PMID:2521882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obaru, K.; Fukuda, M.; Maeda, S.; Shimada, K.
Biochem. 99, 885-894, 1986
Title: A cDNA clone used to study mRNA inducible in human tonsillar lymphocytes by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:M23178; GB:M32337; NID:g182846; PIDN:AAA35858.1; PID:g182847
Accession: A35673; A30574; A30412; A24198; A30908
Nakao, M.; Nomiyama, H.; Shimada, K.
1. Cell. Biol. 10, 3646-3658, 1990
Title: Structures of human genes coding for cytokine LD78 and their expression.
Reference number: A35673; MUID:90287155; PMID:1694014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MOVSTAALAVLLCTMALCNOFSASLAADTPTACCFSYTSROIPONFIADYFETSSOCSKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lross-references: EMBL:U22414; NID:g790632, PIDN:AAA80608.1; PID:g790633
luperfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GB:X03754; NID:g34298; PIDN:CAA27388.1; PID:g758089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 51.9%; Score 248; DB 2; Length 92; 1 Similarity 48.4%; Pred. No. 5.9e-20; 44; Conservative 22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number: A24198; MUID:86223879; PMID:3086300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prophage inflammatory protein-lalpha - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GDB:120368; OMIM:182283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wap position: 17q11-17q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
Residues: 1-92 <ZIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
Residues: 1-92 <BLU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
Residues: 1-92 <OBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
Residues: 1-92 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: I52322
                                                                                                                                                        Accession: A35673
                                                                                                                                                                                                                                                                                                                                                                                           Accession: A30574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A30412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A24198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDB: SCYA3
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A Molecule type: mRNA
A Residues: 1-92 - CBRO.
A ACCOSS-references: GB: M23503; NID:g533244; PIDN:AAA40148.1; PID:g533245
R:Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; M
Mad. 168, 2251-2259, 1988
A.Title: Resolution of the two components of macrophage inflammatory protein 1, and cl.
A.Reference number: JL0088; MUID:89067830; PMID:3058856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             macrophage inflammatory protein 1-beta precursor - mouse
NyAlternate names: H400: SIS gamma; T-cell activation protein gamma
Sydies: Stands musculus (house mouse)
Cypecies: Mus musculus (house mouse)
Cypecies: Mus musculus (house mouse)
Cypecies: Mus 1989 #sequence revision 28-Aug-1989 #text_change 16-Jul-1999
Cypecession: G10552; Jul088; PS0304; S22042
Cypecession: K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J. Immunol. 142, 679-687, 1989
A;Title: A family of small inducible proteins secreted by leukocytes are members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C/Superfamily: macrophage inflammatory protein
C/Reywords: glycoprotein
C/Reywords: glycoprotein
E/1-23/Domain: signal sequence #status predicted <SIG>
E/24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>
E/76/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 24-33, XX7,36, XX,38 <SH2>
Nobabbersies, P.; Lepretre, F.; Bailleul, B.; Grove, M.; Fragnell, I.; Plumb, M. submitted to the RMBL Data Library, October 1991
A;Description: Sequence of the murine macrophage inflammatory protein 1b gene.
                                                                                                                                                     1 MKVSAARLAVILIATALCAPASASPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                              | MKVSTAALAVLLCTMALWNEVFSAPYGADTPTACCFSY-GRQ:PRKFIADYFETSSLCSQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLCVSALSLLLLVAAFCAPGFSAPMGSDPPTSCCFSYTSROLHRSFVMDYYETSSLCSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M35590; NID:g199696; PIDN:AAA39708.1; PID:g199697
A;Accession: PS0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: X62502; NID: 953126; PIDN: CAA44364.1; PID: 953127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 92;
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                                                                            25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s of various activation processes.
A;Reference number: A30552; MUID:89093958; PMID:2521353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
51.9%; Score 248; DB 2;
51.1%; Pred. No. 5.9e-20;
tive 18; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 245.5; DB 2
Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.4%; Scot.
45.7%; Pred. No. 1...
23; Mismatches
                                                                                                                                                                                                                                                                                                          60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                   Comment: This protein is a monokine.
                                                                            47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Conservative
    Query Match
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C.Superfamily: macrophage inflammatory protein C.Keywords: heparin binding F.1-23/Domain: signal sequence #status predicted <SIG> F.24-92/Product: macrophage inflammatory protein #status experimental <MAT> C,Comment: This protein is a monokine. C,Genetics: A,Introns: 23/3; 26/1; 63/2 45; Conservative Query Match Best Local Similarity A; Molecule type: mRNA A; Residues: 1-92 < LIP> A, Molecule type: mRNA A, Residues: 1-92 < CHA> A; Accession: JH0319 A; Accession: A40978 A; Accession: A31767 Accession: A3741 RESULT 9 Db à ઠે Cross-references: EMBL:X53372; NID:954062; PIDN:CAA37452.1; PID:9297531
Notes: the authors: translation of the mucleotide sequence differs at several positions
Kwon, BS.; Wetssman, S.M.
Coc. Natl. Acad. SCi. U.S.A. 86, 1963-1967, 1989
Title: CDNA sequence of two inducible T-cell genes. Accession: A30552
Molecule type: mRNA
Cross-references: GB:M23447; NID:g533240; PIDN:AAA40146.1; PID:g533241
Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Mas
Exp. Med. 168, 2251-2259, 1988
Title: Resolution of the two components of macrophage inflammatory protein 1, and clor
Reference number: JL0088; MUID:89067830; PMID:3058856 Accession: PS0303
Molecule type: mRNA
Molecule: 24-33, 'XX', 36-54 <SHE>
Wolpe, S.D., Davacelis, G.; Sherry, B.; Beutler, B.; Hesse, D.G.; Nguyen, H.T.; Moldaw
Exp. Med. 167, S70-581, 1988
Title: Macrophages secrete a novel heparin-binding protein with inflammatory and neutr
Reference number: A27596; MUID:88154745; PMID:3279154 Residues: 24-33,7XX, 36-42 <WOL>
Note: 26-Met, 30-Pro, and 39-Thr were also found
Note: 26-Met, 30-Pro, and 39-Thr were also found
Midmer, U.; Yang, Z.; van Deventer, S.; Manogue, K.R.; Sherry, B.; Cerami, A.
Immunol. 146, 401-4040, 1991
Title: Genomic structure of murine macrophage inflammatory protein-1-alpha and conserv Cross-references: EMBL:X12531; NID:g53122; PIDN:CAA31047.1; PID:g53123
Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
Immunol. 142, 679-687, 1989
Title: A family of small inducible proteins secreted by leukocytes are members of a ne crophage inflammatory protein-1-alpha precursor - mouse
Alternate names: heparin-binding chemotaxis protein; L2G25B protein; SCI/MIP-la; SIS a
Species: Mus musculus (house mouse)
Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 16-Jul-1999
Accession: S11685; A31393; S05433; A53885; A30522; P60303; A27596; I56104
Grove, M.; Lowe, S.; Graham, G.; Pragnell, I.; Plumb, M.
cleic Acids Res. 18, 5561, 1990
Title: Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammatory
Reference number: S11685; MUID:91016858; FMID:2216738 Title: Cloning and characterization of a cDNA for murine macrophage inflammatory prote Reference number: S04533; MUID:88258380; PMID:3290382 Molecule type: mRNA Residues: 1-48, E', 50-90, I', 92 < DA2> Cross-references: EMBL:X12531 Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue Note: the sequence has been corrected in reference A53885 Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermsen, K.; Luedke, C.; Gallegos, C.; Exp. Med. 170, 2189, 1989 Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermsen, K.; Luedke, C.; Gallegos, C.; Exp. Med. 167, 1939-1944, 1988 Cross-references: GB:J04491; NID:g201524; PIDN:AAA40304.1; PID:g201525 Cross-references: GB:M73061; NID:g199694; PIDN:AAA39707.1; PID:g199695 of various activation processes.
Reference number: A30552; MUID:89093958; PMID:2521353 Reference number: 156104; MUID:91237116; PMID:2033269 Accession: 156104 Title: cDNA sequence of two inducible T-cell genes. Reference number: A32393; MUID:89184547; PMID:2784565 Status: preliminary; translated from GB/EMBL/DDBJ Reference number: A53885 ecule type: protein Accession: A32393 Molecule type: mRNA Residues: 1-92 <KWO> Accession: A53885 Molecule type: mRNA Residues: 1-92 <DAV> Molecule type: DNA Residues: 1-92 <RES> Molecule type: DNA Residues: 1-92 <GRO> Accession: A27596 Molecule type: pro Contents: erratum 804533

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A)Cross-references: GB:X53682; NID:g34217; PIDN:CAA37723.1; PID:g34218
A)Experimental source: natural killer cell, strain CD3-CD2+, F5, 51IE5
K)Appolitano, M.; Modi, W.S.; Cevario, S.J.; Gnarra, J.R.; Seuanez, H.N.; Leonard, W.J.
B.D.I. Chem. 266, 17531-17536, 1931
A)Title: The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/tax responsiv
A)Reference number: A40978; MUID:91373378; PMID:1894635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                macrophage inflammatory protein 1-beta precursor (validated) - human N.Alternate names: cytokine HC21; G-26 protein; H400 homolog; lymphocyte activation geprein 2 (Act-2); T-cell activation protein gamma c;Species: Homo sapiens (man) C;Date: 07-Jun-1990 #sequence_revision 29-May-1998 #text_change 15-Sep-2000 C;Accession: JH91319; A40978; A31767; A37411; B30574; B45817; D30552 K;Baixeras, E.; Roman-Roman, S.; Jitsukawa, S.; Genevee, C.; Mechiche, S.; Viegas-Pequel Immunol. 27, 1091-1102, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Isolation and characterization of a cDNA encoding a putative cytokine which i; Reference number: A37411; MUID:89325421; PMID:2568930
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A;Reference number: A30574; MUID:89140347; PMID:2521882
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A; Residues: 1-14, '8', 16-69, 'G', 71-92 < NNA>
A; Cross-references: GB: M69201; NID: 9178021
A; Note: 15-Ala was also found
R; Libes, M. A.; Napolitano, M.; Jeang, K.T.; Chang, N.T.; Leonard, W.J.
Proc. Natl. Acad Sci. U.S.A. 85, 9704-9708, 1988
A; Title: Identification, cloning, and characterization of an immune activation gene.
A; Reference number: A31767; MUID: 89071764; PMID: 2462251
                                                                                                                                                                                   1 MKVSAARLAVILIATALCAPASASPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                 1 MKVSTTALAVLLCTMTLCNQVFSAPYGADTPTACCFSY-SRKIPRQFIVDYFETSSLCSQ 59
                                                                                            Gaps
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A;Residues: 1-19,1L',21-92 <ZIP>
A;Cross_references: GB:M25316; NID:9602454; PIDN:AAA57256.1; PID:g602455
R;Miller, M.D.; Hata, S.; Malefyt, R.D.W.; Krangel, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Immunol. 27, 1091-1102, 1990
A;Title: Cloning and expression of a lymphocyte activation gene (LAG-1).
A;Reference number: JH0319; MUID:91061800; PMID:2247088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:J04130; NID:g178017; PIDN:AAAS1576.1; PID:g178018 R;Chang, H.C.; Reinherz, E.L.
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R;Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.
J. Immunol. 142, 1582-1590, 1989
Score 243; DB 2; Length 92; Pred. No. 2.1e-19;
                                                                                       26; Indels
                                                                                                                                                                                                                                                                                                                                                                            60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                             60 PGVIFLTKRNRQICADSKETWVQEYITDLELN 91
                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Immunol. 19, 1045-1051, 1989
    50.8%;
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A;Molecule type: DNA
A;Residues: 1-92 <BAI>
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1 MKVSAALLWIJLIAAAFSPQGLTGPASVPTT-CCFNLANRKIPLQRLESYRRITSGKCPQ 59

S

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A;Cross-references: GB:X72308; GB:S57464; NID:g3928270; PIDN:CAA51055.1; PID:g313708 R;Milty, A.; Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Milous Rubmitted to the EMBL Data Library, March 1993 A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoatt:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Comment: This protein induces proteinase secretion and chemotaxis by macrophages and C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rjopdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 131, 535-542, 1993
A.fitle: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA
A,Reference number: JC1478; MUID:93213290; PMID:8461011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 MKASAALLCLLLTAAAFSPQGLAQPVGINTSTTCCYRFINKKIPKQRLESYRRTTSSHCP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKVSAARLAVILIATALCAPASASPYSSDT-TPCCFAYIARPLPRAHIKEY-FYTSGKCS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monocyte chemoattractant protein-1 - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-109 <MIN>
A;Cross-references: EMBL:X71067; NID:g288396; PIDN:CAA50405.1; PID:g288397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein; inflammation
C;Keywords: cytokine; glycoprotein; inflammation
F;1-33/Domain: signal sequence #status predicted <SIG>.
F;34-109/Product: monocyte chemctactic protein 3 #status predicted <MAT>
F;39/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.9%; Score 167; DB 2;
35.2%; Pred. No. 4.5e-11;
tive 23; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 NPAVVFVTRKNROVCANPEKKWVREYINSLE 89
                                                                                                                                                                                                                                                                                        monocyte chemotactic protein 3 precursor - human
                                                                                        60 KAVIFKTKLAKDICADPKKRWVQDSMKYLD 89
                                                     60 PAVVPVTRKNRQVCANPEKKWVREYINSLE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:138473; OMIM:158106
A;Map position: 17q11-17q12
A;Introns: 36/1; 75/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDB:SCYA7; SCYA6; MCP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 35.2% hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:X72309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S32222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-109 <0P2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-109 <OPD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A54678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: JC1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S3222;
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                                                                                                                                                                                                                            RESULT 11
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Molecule type: mRNA
Cross-references: GB:M23502; NID:9533212; PIDN:AAA36656.1; PID:9533213
Clore, G.M.; Lodi, P.J.; Garrett, D.S.; Gronenborn, A.M.
Dmitted to the Brookhaven Protein Data Bank, January 1994
Reference number: A52206; PDB:HUM
Contents: annotation; conformation and disulfide bond assignments by (1)H-NNR, residue
Comment: This protein is secreted by activated lymphocytes and monocytes. It is bound
                                                                                                                                                                                                                                                                                                5
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Title: Human dermal fibroblasts express coctaxin: Molecular cloning, mRNA expression, a Reference number: JC4912; MUID:96374440; PMID:8780731
                                                                                                                            Molecule type: mRNA
Residues: 7-55,'I',57-79,'T',81-92 <MIL>
Cross-references: GB.M57503, NID:g339726; PIDN:AAA36752.1; PID:g339727
Cross-references: GB.M57503, ND:g339726; PIDN:AAA36752.1; PID:g339727
Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
Immunol. 142, 679-687, 1989
Title: A family of small inducible proteins secreted by leukocytes are members of a 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: macrophage inflammatory protein
Keywords: chemotaxis; cytokine; inflammation
1-23/Domain: signal sequence #status predicted <SIG>
24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>
34-58,35-74/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
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Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
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Immunol. 143, 2907-2916, 1989
Title: A novel polypeptide secreted by activated human T lymphocytes. Reference number: A45817; MUID:90038522; PMID:2809212
Accession: B45817
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Comment: This protein has eosinophil specific chemotatic activity.
Superfamily: macrophage inflammatory protein
Keywords: fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 50.7%; Score 242.5; DB 1; Length 92; Local Similarity 45.7%; Pred. No. 2.3e-19; nes 42; Conservative 23; Mismatches 26; Indels 1
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Pred. No. 3.2e-11;
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                                                                                                                                                                                                                                                                                                                        of various activation processes.
Reference number: A30552; MUID:89093958; PMID:2521353
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19-97/Product: eotaxin #status predicted <MAT>
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Best Local Similarity 41.18
Matches 37; Conservative
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Introns: 26/1; 64/2
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Molecule type: mRNA
Residues: 1-97 <BAR>
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Bartels, J.; Schl)
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Matches

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2; Gaps

7

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monocyte chemoattractant protein-1 precursor - pig
C,Species: Sus scrofa domestica (domestic pig)
C,Species: Sus scrofa domestica (domestic pig)
C,Bacession: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999
C;Bacession: JC2136; S57498
C;Accession: JC2136; Money. T; Klaudy, J; Wempe, F; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994
A;Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Ana. A;Reference number: JC2136; MUID:94183284; PMID:7510962
A;Accession: JC2136
A;Molecule type: mRNA
A;Residues: 1-99 < HOS>
A;Cross-references: GB:Z48479; NID:g683716; PIDN:CAA88370.1; PID:g683717
B;Zach.
                                                                A,Accession: JC5295
A,Molecule type: mRNA
A,Residues: 1-99 - VANA
A,Residues: 1-99 - VANA
A,Residues: 1-99 - VANA
A,Cross-references: GB:Y10802, NID:g1924937, PIDN:CAA71760.1; PID:g1924938
A,Experimental source: bone marrow
C,Comment: This protein belongs to the beta-chemokine family which is one of the majo: tis and in tumor biology, and contribute to the trafficking and recuitment of the resiculations:
Biochem. Biophys. Res. Commun. 231, 726-730, 1997
A,Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression
A,Reference number: JC5295; MUID:97224420; PMID:9070881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKVSAARLAVILIATALCAPASASPYS-SDTTPCCFAYIARPLPRAHIKEYF-YTSGKCS 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:1-23/Domain: signal sequence #status predicted <SIG>F:24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, July 1994
A;Reference.number: S57497
A;Accession: S57498
A;Accession: S57498
A;Actus preliminary
A;Molecule type: mRNA
A;Residues: 1-99 < ZAC>
A;Cross-references: EMBL:X79416; NID:g872312; PIDN:CAA55945.1; PID:g872313
C;Keywords: glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 32.4%; Score 155; DB 2; Length 99 Local Similarity 37.4%; Pred. No. 8.4e-10; Nes 34; Conservative 20; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KEAVIFKTIAGKEICAEPKOKWVODSISHLD 91
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Cross-references: BMBLX17053; NID:g55530; PIDN:CAA34901.1; PID:g55531
Cross-references: EMBLX17053; NID:g55530; PIDN:CAA34901.1; PID:g55531
XOshimura, T.; Takeya, M.; Takahashi, K.
iochem. Biophys. Res. Commun. 174, 504-509, 1991
inchem. Biophys. Res. Commun. 174, 504-509, 1991
inchem. Biophys. Res. Commun. 174, 504-509, 1991
inchem. Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its exp. Reference number: JN0128; MUID:91128376; PMID:1704226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Accession: JC5295
;Van Coillie, E.; Froyen, G.; Nomiyama, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van Da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Rattus norvegicus (Norway rat)
Date: 10-Sep-1999 #text_change 10-Sep-1999
Accession: S07723, JN0128
Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Aclas Res. 18, 23-34, 1990
Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential
Reference number: S07723, MUID:90174947; PMID:2106664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-148 <YOS>
(Cross-references: GBMS)7441; NID:g205333; PIDN:AAA63496.1; PID:g205334
(Experimental source: spleen cells
(Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: macrophage inflammatory protein;1-23/Domain: signal sequence #status predicted <SIG>;1-23/Domain: signal sequence #status predicted <MAT>;24-148/Product: immediate-early serum-responsive protein JE #status predicted <WAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEY-FYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MORSSVLLCLLVIEATFCSLLMAQPDGVNTPTCCYTF-NKQIPLKRVKGYERITSSRCPQ 59
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;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
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                                                                                                                                                      Cross-references: GB:L04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
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                                                                                                                                                                                                                                                                                                                            / Match 120; Score 162; DB 2; Length 120; Local Similarity 35.6%; Pred. No. 1.7e-10; Los 32; Conservative 21; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nmediate-early serum-responsive protein JE precursor - rat Alternate names: monocyte chemoattractant protein-1
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                          Accession: I48147
Status: preliminary; translated from GB/EMBL/DDBJ
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Residues: 1-120 <RES>
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                                                                                                             December 16, 2003, 15:36:20 ; Search time 10.4426 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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SEQUENCE FROM N.A.
MEDLINE=99228475; PubMed=10213461;
Nomiyama H., Fukuda S., Iio M., Tanase S., Miura R., Yoshie O.;
"Organization of the chemokine gene cluster on human chromosome
17q11.2 containing the genes for CC chemokine MPIF-1, HCC-2, LEC, and

Jang J.S., Kim B.E.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

SECUENCE FROM N.A.

SEQUENCE FROM N.A.
Zeng Q.P., Yang R.Y., Fu L.C.;
"The complete sequence of human beta-chemokine RANTES mRNA.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

Interferon Cytokine Res. 19:227-234(1999).

TISSUE=Brain,

RA MEDLINE=22388257; PubMed=12477932;

RA Altachul S.F., Collins F.S., Wagner L.H., Derge J.G., Schuler G.D.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hochul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Wang J., Wang L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Parage C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hilyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

34 152 31.8 99 1 SY02 PIG 000626 homo sapien 150.5 31.5 93 1 SY02 PIG 000626 homo sapien 150.5 31.4 99 1 SY02 BUVIN P82443 bos taurus 37 150 31.4 99 1 SY08 BOVIN Q09141 bos taurus 38 146.5 30.6 148 10.1 8Y02 MOUSE P48298 mus muscullu 144 30.1 99 1 MCPA_BOVIN P828291 bos taurus 41 144 30.1 99 1 MCPA_BOVIN P828291 bos taurus 42 143.5 30.0 199 1 MCPA_BOVIN P828291 bos taurus 43 142 29.7 96 1 BCPA_CANPA P49973 sus scroft 44 140 29.3 99 1 SY02_MUSE P80325 cavia porce 44 140 29.3 99 1 SY02_MUSH P93829 sus scroft 44 140 29.3 99 1 SY02_MUSH P93829 cavia porce 44 140 29.3 99 1 SY02_MUSH P93829 cavia porce 57 1 SY02_MUSH P9383 cavia porce 57 1 SY03_MUSH P9383 cavia porce 57 1 SY03_M
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us-09-920-137a-8.rsp

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-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS: CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES BOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
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-:- TISSUE SPECIFICTY: T-CELL AND MACROPHAGE SPECIFIC.
-:- INDUCTION: BY mitogens.
-:- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
Hoover D.M., Shaw J., Gryczynski Z., Proudfoot A.E.I., Wells T.N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells."; Science 270:1811-1815(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99111238; PubMed=9889151, Wilken J., Hoover D., Thompson D.A., Barlow P.N., McSparron H., Picard L., Mlodawer A., Lubkovski J., Kent S.B.; Trotal chemical synthesis and high-resolution crystal structure of the potent anti-HIV protein AOP-RANTES."; Chem. Biol. 6:43-51(1999).
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                                                                                                                                                                                                                                                                                                                         MEDLINE=96106406; PubMed=8525373;
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chung C.-W., Cooke R.M., Proudfoot A.E.I., Wells T.N.C., "The three-dimensional solution structure of RANTES.";
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                                                                                                                                                              human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                      SEQUENCE OF 49-56; 71-79 AND 83-91, AND FUNCTION.
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Biochemistry 34:5329-5342(1995).
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1RTN; 03-JUN-95.
1RTO; 03-JUN-95.
1B3A; 23-APR-99.
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"The crystal s
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPL?RAHIKEYFYTSGKCSNP 60
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P94772; 009076;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 31, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
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Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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                                        MILLY, ACCOUNTY, TAS.

R GO; GO:0008009; F:chemokine activity; TAS.

R GO; GO:0008009; F:chemokine activity; TAS.

R GO; GO:0008009; F:chemokine activity; TAS.

R GO; GO:0006914; P:callum ion homeostasis; TAS.

R GO; GO:0006928; P:call adhesion; TAS.

R GO; GO:0006928; P:call motility; TAS.

R GO; GO:0006989; P:calluar defense response; TAS.

R GO; GO:0006989; P:chemotaxis; TAS.

R GO; GO:0006989; P:inflammatory response; TAS.

R GO; GO:0006959; P:inflammatory response; TAS.

R GO; GO:0006959; P:response to oxidative stress; TAS.

R GO; GO:0006951; P:response to viruses; TAS.

R GO; GO:0006915; P:response to viruses; TAS.

R GO; GO:0007615; P:response to viruses; TAS.
                                                                                                                                                                                                                                                                                                                           SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 472; DB 1; Length 91;
Pred. No. 7.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             SMALL INDUCIBLE CYTOKINE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> R (IN REF. 1 AND 4).
-> V (IN REF. 4).
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              HGNC:10632; CCL5.
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PDB; 1EQT; 19-APR-00
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CONFLICT
STRAND
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                                       AGAIO K., Makamura M., Oguma T., Fukunaga K., Ishizaka A.,
Yamaguchi K., Kanazawa M.;
Yamaguchi K., Kanazawa M.;
Submitted (APPT.1997) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: CHEWOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
-!-SUBCELLULAR LOCATION: Secreted.
-!-SUBCELLULAR LOCATION: Secreted.
-!-SUBCELLULAR LOCATION: Secreted.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A5 precursor (CCLS) (T-cell specific RANTES protein) (SIS-delta).
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Aust G., Thamm B., Rost A.K.;
Aust G., Thamm B., Rost A.K.;
"Cloning of Bos taurus RANIES, mRNA.";
"Cloning of Bos taurus RANIES
"Cloning of MAR.1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, ABUUZDOZ,
HSSP, ABUUZDOZ,
HSSP, PI3501, 1RTN.
InterPro; IRR01081; Chemkine_sml.
InterPro; IRR01081; Chemokine_ID8.
Pfam, PPRO048; IL8, IL.
PROMO48; IL8, IL8, IL8, IL8
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; T-cell; Signal, Inflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 416; DB 1; Length 91;
Pred. No. 1.3e-39;
2; Mismatches 10; Indels
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SEQUENCE FROM N.A.
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CCLS OR SCYAS.
                        IISSUE=Lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKVSATAFAVLLMAAALCAPASASPYASDTTPCCFAYISRPLPRTHVQEYFYTSSKCSMA 60
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of cDNA from renal tubular epithelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta) (MuRantes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=94132613; PubMed=7507961;
Danoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSTIE: PS00472; SMALL CYTOKINES CC; 1.

Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response. SIGNAL 1 23 POTENTIAL.

CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5. DISULFID 33 57 BY SIMILARITY.

DISULFID 34 73 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.5%; Score 404; DB 1; Length 91; 80.2%; Pred. No. 2.7e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92277990; Pubmed-1375672;
Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
Krensky A.M., Neilson E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660DD38E015B0735 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AVVFITRKKROVCANPEKKWVREYINALELS 91
                                                                                                                                                                                                                                                                                                EMBL; AJ007043; CAA07430.1; -.
HSSP; P13501; 1RTN.
InterPro; IPR00827; CC_chemkine_sml.
InterPro; IPR001811; Chemckine_ILB.
Pfon; PF00048; ILB; 1.
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34 73
91 AA; 10073 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 80.2:
hes 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                             C-C) (CHEMOKINE CC).
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SEQUENCE
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runcuelly bobbelly
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runcuelly runcuelly bult C., Runcuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Rosdami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P. Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbania L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Kanal A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Oxido T., Perrea G., Percea G., Percovsky N., Pontius J.U., Qi. Perrea G., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sulana R., Takenska Y., Taylor M.S., Teasadale R.D., Tomada K.,
Sulana R., Analested C., Wang Y., Watanabe Y., Walls C.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
Yuan Z., Zavolan M., Zau Y., Zimmer A., Rakawa T., Fukuda S.,
Hirozane Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakasi D., Sakai K., Sasaki K., Sasaki K., Sasaki K., Sasaki K., Sasaki K., Sasaki A., Sakai K., Sasaki C., Tofull Lengthe M. DNAs.",
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full Lengthe DNAs.",
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full Lengthe M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence polymorphisms in the chemokines Scyal (TCA-3), Scya2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for each, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelltis.", J. Immunol. 163:2262-2266(1999).
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.E., Jordon H., Moore T., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Organization of the mouse CC chemokine cluster containing the genes
"Cloning, genomic organization, and chromosomal localization of the ScyaS gene encoding the murine chemokine RANTES."; J. Immunol. 152:1182-1189(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=B10.S/J, BALB/CJ, DBA/2J, NOD/LTJ, and SJL/J; TISSUE=Spleen, MEDLINE=99370037; PubMed=10438970; Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W., Blankenhorn E.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                        "Definition of a lipopolysaccharide-responsive element in the 5'-flanking regions of MuRantes and crg-2.";
Mol. Cell. Biol. 14:2914-2925(1994).
                                                                                                                                                                                                                                                                                                                                       Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                STRAIN=BALB/c;
MEDLINE=94217689; Pubmed=7513046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Mammary gland;
PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Mazny D.M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnertled Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELI-
CELLS AND BOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
BASOPHILS AND ACTIVATES EOSINOPHILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
SIGNAL
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A -> E (IN REF. 1).
SDFD66F4684FE1C8 CRC64;
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BY SIMILARITY
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MGD; MGI:98262; CC15.
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR001811; Chemokine ILB.
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AF065945; AAC17512.1;

AF065947; AAC17513.1;

AF065947; AAC17514.1;

AF128187; AAF22528.1;

AF061897; AAF2256.1;

AR001101; BAB1871.1;

BC033508; AAH33508.1;
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91 AA; 10071 MW;
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79.1%;
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EMBL, S37648, AAB22330.1, -.
EMBL, U02298, AAA18302.1, -.
EMBL, X70675, CAA50011.1, -.
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EMBL;
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                    &$\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\fra
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RESULT

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SY04 RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKVS-AARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKISAAASLITVILVAAALCTPVPASPYGSDITPCCFAYLSLALPRAHVKEYFYTSSKCSN 60
                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
5mall inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES CCL5 OR SCYA5.
                               01-07-1996 (Rel. 34, Created)
01-07-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A5 precursor (CCLS) (T-cell specific RANTES protein) (SIS-delta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sigmodon hispidus (Hispid cotton rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIGNI FROUDS: SCY: 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.2%; Score 383.5; DB 1; Length 92; 78.3%; Pred. No. 5.3e-36; tive 7; Mismatches 12; Indels ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
B4FBEC2B4208ABC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LAVVFVTRRNRQVCANPEKKWVQEYINYLEMS 92
92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, U06436; AAA96499.1; -.
HSSP; P13501; 1RTN
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR01011; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 58 E
35 74 E
92 AA; 10170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
  STANDARD;
                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-C) (CHEMOKINE CC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               est Local Similarity atches 72; Conserv
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                CCLS OR SCYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKISAAVLTVVLMAASLCAPASASPNGSDTIPCCFAYLSAVLPRAHVKFYFYTSSKCSNF 60
                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).
CCL4 OR SCYA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blanco J.C., Pletneva L.M., Prince G.A.;
"Sigmodon hispidus cytokines, chemokines and interferons.";
Submitted (SEP-2001) to the EMBL/GenBank/DDSJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryccolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%; Score 372; DB 1; Length 91; 75.6%; Pred. No. 1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. SMALL INDUCIBLE CYTOKINE AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DODGEAEABE4242FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AVVFVTRKNRQVCANPEKKWVREYINSLEM 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AVVFVTRRNRQVCANPKKKWVQEYINYLEL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBD; AF421391; AAL16932.1; -. InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_LL8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID 33 57 F
DISULFID 34 73 F
SEQUENCE 91 AA; 10082 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00048; IL8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 68; Conserv
                                                          SECUENCE FROM N.A.
                  NCBI_TaxID=42415;
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1 MKVSAARLAVILIATALCAPASASPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
MEDLINE=90287155; PubMed=1694014;
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HSSP; P13236; 1HUM.
Genew; HGNC:10628; CCL3L1.
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Best Local Similarity
                                                                                                                                                                             SEQUENCE FROM N.A.
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      SOTETTE TO DESCRIBE TO DE DESCRIBE TO D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-91103879; PubMed=2271120;
MEDLINE-91103879; PubMed=2271120;
MIThree human homologs of a murine gene encoding an inhibitor of stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SY3L HUMAN STANDARD, PRT; 93 AA.
P16619; Q96168;
D14AG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A3 like 1 precursor (Tonsillar lymphocyte LD78 beta protein) (G0/G1 switch regulatory protein 19-2) (G0S19-2 protein) (PAT 464.2).
CCL3L1 OR SCYA3L1 OR G0S19-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Irving S.G., Zipfel P.F., Balke J., McBride O.W., Morton C.C., Burd P.R., Siebenlist U., Kelly K.; "Two inflammatory mediator cytokine genes are closely linked and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SÍMILAŘITY.
SMALL INDUCIBLE CYTOKINE A4.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECBA8818D42A735C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.2%; Score 254.5; DB 1
51.1%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PAVVFQTKKGRQVCANPSESWVQEYVDDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00472; SMALL CYTOKINES CC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variably amplified on chromosome 17q." Nucleic Acids Res. 18:3261-3270(1990).
                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P13236, 1HUM.
InterPro, IPR000827; CC_chemkine_sml.
InterPro, IPR001811; Chemokine_IL8.
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34 58
34 58
35 74
92 AA; 10066 MW;
                                                                                                                                                                                                                                                                                                                                                       EMBL; D17402; BAA04226.1; -. PIR; I46730; I46730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Juery Match
3est Local Similarity 51.1%
fatches 47; Conservative
                                                                 C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine; Chemotaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31. HUMAN
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                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
--- SUBCELLUAR LOCATION: Secreted.
--- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C.) (CHEMOKINE CC). STRONG, TO SCYA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMALL INDUCIBLE CYTOKINE A3 LIKE 1.
Nakao M., Nomiyama H., Shimada K.; "Structures of human genes coding for cytokine LD78 and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 252.5; DB 1; Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 23 SMALL INDUCIBLE CYTOKINE A3 L. 34 58 BY SIMILARITY. 35 74 BY SIMILARITY. 91 91 91 L -> P (IN REF. 4; AAH07783). 93 AA, 10161 MW; A7A79E774006D61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; Provoso, -CX; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES_CC; 1.
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N
                                              Mol. Cell. Biol. 10:3646-3658(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X52149; CAA36397.1; -.
EMBL, M24110; AAA35859.1; -.
EMBL, D90145; BAA14173.1; -.
EMBL, BCC007783; AAH07793.1; -.
EMBL, BCC027888; AAH07783.1; -.
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SY03 HUMAN
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-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                        0908365; 0910C9, 001.000-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A4 homolog precursor (Macrophage inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95369710; Pubmeu='o=++++, Petrenko O., Ischenko I., Enrietto P.J.; Petrenko O., Ischenko I., Enrietto Protein-I peta."; Gene 160:305-306(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A. Hughes S.M., Bumstead N.; Hughes S.M., bumstead N.; Hughes S.M., bumstead N.; amain mapping of the gene encoding the chicken homologue of the mammalian chemokine SCYA4."; chemokine SCYA4."; cubmitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE OF 14-90 FROM N.A.
PECTRANKO O., Enrietto P.J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMALL INDUCIBLE CYTOKINE A4 HOMOLOG. BY SIMILARITY. BY SIMILARITY.
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                                                                                          60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                       61 PSVIFLTKRGRQVCADPSEEWVQKYVSDLELS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                            90 AA.
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Cytokine; Chemotaxis; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P13236; 1HUM.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IRR001811; Chemokine_Ibs.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINE=95369710; PubMed=7642115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L34553; AAA48747.1; -.
EMBL; AJ243034; CAB45103.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lus gallus (Chicken).
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72
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 1-beta homolog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
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Query Match

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5
                                              1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLFRAHIKEYFYTSGKCSN 59
                                                                                 1 MKVSVAALAVLII--AICYQTSAAPVGSDPPTSCCFTYISRQLPFSFVADYYETNSQCPH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49.

MEDLINE=96127783; PubMed=8541527;

Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S.,

Czaplewski L.G., Dexrer T.M., Drummond A.H., Gearing A.H.,

Heyworth C.M., Lord B.I., Mccourt M., Varley P.G., Wood L.M.,

Bedwards R.M., Lewis P.J.;

"BB-10010: an active variant of human macrophage inflammatory protein-
1 alpha with improved pharmaceutical properties.";
                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
protein l-alpha) (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha
protein) (G0/G1 swirch regulatory protein 19-1) (G0S19-1 protein)
(SIS-beta) (PAT 464.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91103879; PubMed=2271120;
MEDLINE=91103879; PubMed=2271120;
Blum S., Forsdyke R.E., Forsdyke D.R.;
"Three human homologs of a murine gene encoding an inhibitor of stem
                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.; Mitogenic activation of human T cells induces two closely related genes which share structural similarities with a new family of secreted factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakao M., Nomiyama H., Shimada K.;
"Structures of human genes coding for cytokine LD78 and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Obaru K., Fukuda M., Maeda S., Shimada K.;
"A cDNA clone used to study mRNA inducible in human tonsillar lymphocytes by a tumor promoter.";
J. Biochem. 99:885-894(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jang J.S., Kim B.E.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
Best Local Similarity 51.1%; Pred. No. 2.6e-21;
Matches 47; Conservative 19; Mismatches 23; Indels
                                                                                                                           60 PAVVFVTRKNRQVCANPEKKMVREYINSLEMS 91
                                                                                                                                                  92 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 10:3646-3658(1990).
                                                                                                                                                                                                                                                           PRT;
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MEDLINE=90287155; Pubmed=1694014;
                                                                                                                                                                                                                                                                                                                                                                                                                        OR SCYA3 OR G0S19-1 OR MIPIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=89140347; PubMed=2521882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=86223879; PubMed=3086300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blood 86:4400-4408(1995)
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
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Genew, HGNC.10627; CCL3.

MIM, 182283; --
GO; GO:0003805; F:acluble fraction; TAS.
GO; GO:0003806; F:antiviral response protein activity; TAS.
GO; GO:000809; F:chemokine activity; TAS.
GO; GO:0006804; F:signal transducer activity; TAS.
GO; GO:0006804; P:calcium ion homeostasis ras.
GO; GO:0006804; P:calcium ion homeostasis; TAS.
GO; GO:0006804; P:call-call signaling; TAS.
GO; GO:0006804; P:cell-call signaling; TAS.
GO; GO:000695; P:chemotaxis; TAS.
GO; GO:000695; P:chemotaxis; TAS.
GO; GO:000695; P:inflammatory response; TAS.
GO; GO:0007011; P:regulation coupled receptor protein signalin. .; TAS.
GO; GO:0007011; P:regulation Go; GO:000695; P:inflammatory response; TAS.
GO; GO:0007011; P:regulation Go; GO:000695; P:inflammatory response; TAS.
GO; GO:0007011; P:regulation TAS.
GO; GO:0007011; P:regulation; TAS.
GO; GO:000816; P:signal realication; TAS.
InterPro; IPRO00821; CC_chemkine_sml.
InterPro; IPRO00821; CC_chemkine_sml.
InterPro; IPRO01811; Chemokine_iDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMML outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Indentification of RANTES, MIP-1 alpha, and MIP-1 beta as the major
HIV-suppressive factors produced by CD8+ T cells.";
Science 270:1811-1815 (1995).

"Indentification of RANTES (1995).

"Indentification of CCR1 CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE
FUNCTION: MONOKINE WITH INFLAWMATORY AND CHEMOKINETIC PROPERTIES.

BINDS TO CCR1 CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE
FRACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-ALPHA INDUCES
A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2,
AND SIMIAN INMUNOBERICIENCY VIRUS (SIV).

"INDUCTION: BY TOAN OR PHA (TPA = 12-O-TETRADECANOYL PHORBOL-13
ACETATE (TUMOR PROMOTER); PHA = PHYTOHEMAGGLUTININ (T-CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC). STRONG, TO SCYABL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMOO199; SCY; 1.
PROSITE; PSO0472; SMALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
SIGNAL 1 23
                          Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%; Score 248; DB 1; Length 92; 48.4%; Pred. No. 6.5e-21; tive 22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D->A: IN BB-10010; IMPROVED PHARMACEUTICAL PROPERTIES.
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BY SIMILARITY
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PIR; A35673; A30574.
PDB; 1B50; 22-JUL-99.
PDB; 1B53; 22-JUL-99.
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nes 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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Conservative

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                             1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Secreted.
-:- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS).
-:- SIMILARITY: BELCNGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
CCL3 OR SCYA3 OR MIP1A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INJURY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Makagawa H., Shiota S., Takano K., Shibata F., Kato H.;
Makagawa H., Shiota S., Takano K.,
"Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
member of rat GRO/CINCs, is a predominant chemokine produced by
lipopolysaccharide-stimulaed rat macrophages in culture.";
lipopolysaccharide-stimulaed rat macrophages in culture.";
HAS CHEMOTACTIC ACTIVITY FOR MONOCYTES, NEUTROPHILS.
HAS CHEMOTACTIC ACTIVITY FOR MONOCYTES, NEUTROPHILS.
BASOPHILS, AND LYMPHOCYTES. REQUIRED FOR LUNG TNF-ALPHA
PRODUCTION, NEUTROPHIL RECRUITMENT AND SUBSEQUENT LUNG INJURY AND
MAY FUNCTION AS AN AUTOCRINE MEDIATOR FOR THE MACROPHAGE
PRODUCTION OF THE-ALPHA WHICH IN TURN UP-REGULATES VASCULAR
APPLESION MOLECULES REQUIRED FOR NEUTROPHIL INFLUX. THIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shi M.M., Godleski J.J., Paulauskis J.D.; "Molecular cloning and posttranscriptional regulation of macrophage inflammatory protein-1 alpha in alveolar macrophages."; Biochem. Biophys. Res. Commun. 211:289-295(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-LONG Evans; TISSUE-Lung;
MEDLINE-95238980; PubMed-7722328;
Shanley T.P., Schmal H., Friedl H.P., Jones M.L., Ward P.A.;
"Role of macrophage inflammatory protein-1 alpha (MIP-1 alpha) in
                                                                                          61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                     61 GVIFLTKRSRQVCADPSEEWVQKYVSDLELS 91
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96183056; PubMed=8607872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95298037; PubMed=7779098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute lung injury in rats.";
J. Immunol. 154:4793-4802(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U22414; AAA80608.1; -.
ERMBL; U06435; AAA96498.1; -.
PIR; I52322; I5322.
HSSP; P13236; 1HUM.
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEOUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lung;
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                                                                                                                                                                                                                                                                                                                                           1 MKVSTAALAVLLCTMALWNEVFSAPYGADTPTACCFSY-GRQIPRKFIADYFETSSLCSQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G., "A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2).
                     Pfam; PF00048; ILB; 1. SMART; SM00199; SCY; 1. PR051TE; PS00472; SMALL CYTOKINES CC; 1. CYCKine; Chemotaxis; Inflammatory response; Signal; Heparin-binding. SIGNAL
                                                                                                                                                                                                                                                                             2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G., Wolpe S.D., Masiarz F., Coit D., Cerami A.;
"Resolution of the two components of macrophage inflammatory protein 1, and cloning and characterization of one of those components, macrophage inflammatory protein 1 beta.";
J. Exp. Med. 168:2251-2259(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;
MEDLINE=99370037; PubMed=10438970;
Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
Blankenhorn E.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence polymorphisms in the chemokines Scyal (TCA-3), Scya2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=DBA/2J; TISSUE-Liver;
Daubersies P., Lepretre F., Bailleul B., Grove M., Pragnell I.,
                                                                                                                                                                                                                                        51.9%; Score 248; DB 1; Length 92; 51.1%; Pred. No. 6.5e-21;
                                                                                                                                                                                                                                                                           25; Indels
                                                                                                                       SMALL INDUCIBLE CYTOKINE A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    A -> T (IN REF. 2).
C -> W (IN REF. 2 AND 3).
14E861C647F9A2EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                  60 PGVIFLTKRNRQICADPKETWVQEYITELELN 91
                                                                                                                                                                                                                                                                           18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 AA
                                                                                                                                   BY SIMILARITY
BY SIMILARITY
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
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MEDLINE=89093958; PubMed=2521353;
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MEDLINE=89067830; PubMed=3058856;
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                                                                                                                                                                                     57 57 67 92 AA; 10335 MW;
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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73
6
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                                                                                                                                                                                                                                                           Similarity
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P14097;
                                                                                                                                                                                                                                                                         47;
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DISULFID
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CONFLICT
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
8mall inducible cytckine A3 precursor (CL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (Heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
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Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermsen K., Luedke C., Calalegos C., Coit D., Merryweather J., Cerami A.;
"Cloning and characterization of a cDNA for murine macrophage inflammatory protein (MIP), a novel monokine with inflammatory properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.4%; Score 245.5; DB 1; Length 92; 45.7%; Pred. No. 1.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMALL INDUCIBLE CYTOKINE A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8853FD58FDE61BAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; Chemotaxis; Inflammatory response; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PAVVFLTKRGRQICANPSEPWVTEYMSDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:98261; CC14.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF128218; AAF22559.1; -. EMBL; AF128219; AAF22560.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M23503; AAA40148.1; -.
EMBL; M35590; AAA39708.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X62502; CAA44364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Conservative
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                                                                                                                                                                                   C-C) (CHEMOKINE CC)
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84
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"Sequence polymorphisms in the chemokines Scyal (TCA-3), Scya2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for each, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis."; J. Immunol. 163:2266-2266(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, AND PANCREAS.
SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic structure of murine macrophage inflammatory protein-1 alpha and conservation of potential regulatory sequences with a human homolog, LD78.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolpe S.D., Davatelis G., Sherry B., Beutler B., Hesse D.G.,
Nguyen H.T., Moldawer L.L., Nathan C.F., Lowry S.F., Cerami A.;
"Macrophages secrete a novel heparin-binding protein with
inflammatory and neutrophil chemokinetic properties.",
J. Exp. Med. 167:570-581(1988)
-!- FUNCTION: MONKINE WITH INFLAMMATORY, PYROGENIC AND CHEMOKINETIC
PROPERTIES. HAS A POTENT CHEMOTACTIC ACTIVITY FOR EOSINOPHILS.
BINDING TO A HIGH-AFFINITY RECEPTOR ACTIVATES CALCIUM RELEASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/CJ, DBA/2J, NOD/LTJ, SJL/J, and B10.S/J; TISSUE=Spleen; MEDLINE=99370037; PubMed=10438970; Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
                                                                                                                                                                                                                                                                                                                                                             Grove M., Lowe S., Graham G., Pragnell I., Plumb M., "Sequence of the murine haemopoietic stem cell inhibitor/macrophage
                                               Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermsen K., Luedke C., Gallegos C., Coit D., Merryweather J., Cerami A.;
J. Exp. Med. 170:2189-2189(1989).
                                                                                                                                                                Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
"A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.";
J. Immunol. 142:679-687(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91237116; PubMed=2033269;
Widmer U., Yang Z., van Deventer S., Manogue K.R., Sherry B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kwon B.S., Weissman S.M.; "cDNA sequences of two inducible T-cell genes."; Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory protein 1 alpha gene.";
Nucleic Acids Res. 18:5561-5561(1990)..
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MEDLINE=88154745; PubMed=3279154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=89184547; PubMed=2784565;
                                                                                                                                                    MEDLINE=89093958; PubMed=2521353;
                                                                                                                                                                                                                                                                                                                                               MEDLINE=91016858; PubMed=2216738;
Exp. Med. 167:1939-1944(1988).
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                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                            STRAIN=DBA/2J;
                                       REVISIONS.
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1 MKVSAARLAVILIATALCAPASASPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
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Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;
"Mitogenic activation of human T cells induces two closely related
genes which share structural similarities with a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89071764; PubMed=2462251;
Lipes M.A., Napolitano M., Jeang K.-T., Chang N.T., Leonard W.J.;
Identification, cloning, and characterization of an immune
activation gene.";
Proc. Natl. Acad. Sci. U.S.A. 85:9704-9708(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Indels
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34 57 BY SIMILARITY.
35 73 BY SIMILARITY.
22 22 F -> L (IN REF. 3).
62 62 V -> A (IN REF. 3).
92 AA; 10345 MW; 8BFF2DE7C6DEDD38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; iravil.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
PROSITE: P-Anonctaxis; Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphocyte-secreted protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity; IDA
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InterPro; IPR001811; Chemokine_IL8
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                                  EMBL, M23447; AAA40146.1; -
EMBL, X53372; CAA31047.1; -
EMBL, X53372; CAA314452.1; -
EMBL, J04491; AAA40304.1; -
EMBL, A73061; AAA39707.1; -
EMBL, AF06599; AAC17507.1; -
EMBL, AF065941; AAC17507.1; -
EMBL, AF065941; AAC17508.1; -
EMBL, AF065942; AAC17508.1; -
EMBL, AF065942; AAC17508.1; -
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GO:0008009, F:chemokine
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HSSP; P13236; 1HUM.
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[3] SEQUENCE FROM N.A. Mosmann T.R., Zurawski G.; MEDLINE=89091958; PubMed=2521353; Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.; Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.; Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.; Aramily of small inducible proteins secreted by leukocytes are memberase of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by multidimensional NMR.";
Science 263:1762-1767(1994).
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERSIVE
BINDS TO CRES AND TO CCRS. ONE OF THE MAJOR HIV-SUPPRESSIVE
FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-BETA INDUCES A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The gene encoding the Act-2 cytokine. Genomic structure, HTLV-1/Tax responsiveness of 5' upstream sequences, and chromosomal
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MEDLINE=91061800; PubMed=2247088;
BAIXETAS E., Roman-Roman S., Jitsukawa S., Genevee C., Mechiche S., Viegas-Pequignot E., Hercend T., Triebel F.;
Viegas-Pequignot E., Hercend T., Triebel F.;
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Mol. Immunol. 27:1091-1102(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang H.C., Reinherz E.L.;
"Isolation and characterization of a cDNA encoding a putative cytokine which is induced by stimulation via the CD2 structure on human T lymphocytes.", Eur. J. Immunol. 19:1045-1051(1989).
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Miller M.D., Hatta S., Waal Malefyt R., Krangel M.S.;
"A novel polypeptide secreted by activated human T lymphocytes.";
J. Immunol. 143:2207-2216(1989).
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Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
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MEDINE=98180363, Pubmed=9521068,
BERTNARDIN G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
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Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P.,
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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Biol. Chem. 266:17531-17536(1991).
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MEDLINE=91373378; Pubmed=1894635;
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TISSUE=T-cell;
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                                        -i- INDUCTION: By mitogens.
-i- SIMILARITY: BELDONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHENOKINE CC).
DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00048; ILB; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMALL INDUCIBLE CYTOKINE A4.
BY SIMILARITY.
BY SIMILARITY.
T -> C (IN REF. 7).
P -> L (IN REF. 5).
P -> L (IN REF. 5).
ARKLPR -> REASS (IN REF. 3).
S -> I (IN REF. 6).
S -> G (IN REF. 6).
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                                                                                                                                                                              1, J04130; AAA51576.1; -.
1, X55881; CAA37723.2; ALT_SEQ.
1, X16166; CAA374291.1; -.
1, M62203; AAB00790.1; -.
1, M62203; AAB00790.1; JOINED.
1, M65201; AAB00790.1; JOINED.
1, M65202; AAB00790.1; JOINED.
                               SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                            EMBL; M23502; AAA36656.1; -.
EMBL; M25316; AAA57256.1; -.
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PDB; 1HUN; 30-APR-94.
PDB; 1JE4; 03-OCT-01.
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                                                                                                                                                                                        EMBL; X53683;
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                                                                                        1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-F8B-2003 (Rel. 41, Last annotation update)
Small inducible cytckine A4 precursor (CCL4) (Macrophage inflammatory
CCL4 OR SCYA4 OR MIP1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                    Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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47.8%; Score 228.5; DB 1; Length 92;
Best Local Similarity 42.4%; Pred. No. 9.7e-19;
Matches 39; Conservative 22; Mismatches 30; Indels 1
  DB 1; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMALL INDUCIBLE CYTOKINE A4. BY SIMILARITY. BY SIMILARITY.
                                                 23; Mismatches 26; Indels
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34 58 BY SIMILARITY.
35 74 BY SIMILARITY.
92 AA; 10234 MW; 60B451EEEEC7103D CRC64;
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InterPro; IPR000811; Chemokine_ILB.
Bara; PF000048; ILB.; SWARI; SM00199; SCY; I.
PROSITE; PS00472; SMALL_CYTOKINES_CC; I.
CYTOKINE; Chemotaxis; Inflammatory response; Signal.
SIGNAL
50.7%; Score 242.5; DB 1
45.7%; Pred. No. 2.7e-20;
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                                                                                                                                                                                              60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                             61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
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     Query Match
Best Local Similarity
Matches 42; Conserv
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P50230;
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Search completed: December 16, 2003, 15:38:22
Job time : 11.4426 secs
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December 16, 2003, 15:36:20; Search time 30.3333 Seconds (without alignments) 774.158 Million cell updates/sec
                                                                                                                                                                                  1 MKVSAARLAVILIATALCAP......VCANPEKKWVREYINSLEMS 91
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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quence: 1 MK
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_rodent:*
sp_virus:*
sp_virus:*
sp_vortebrate:*
sp_vortebrate:*
sp_rovirus:*
sp_rovirus:*
sp_bacteriap:*

SUMMARIES

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Description	Q8hyq1 macaca mula	Q8mkd0 equus cabal	Q8hys0 canis famil	Q8sg40 felis silve	Q8qq57 qallus qall	Q8hyn5 macaca mula	Q8sga6 bos taurus	Q8hyd3 macaca mula	Q8hyg2 macaca mula	O9pwa6 gallus gall	Q91z10 Bigmodon hi	Q91z65 sigmodon hi	Q8nhw4 homo sapien	Q14745 homo sapien	Q9i8e0 qallus qall	Q8q956 gallus gall	
Ω Η	Q8HYQ1	Q8MKD0	Q8HYS0	Q8SQ40	080057	Q8HYN5	Q8SQA6	Q8HYQ3	Q8HYQ2	Q9PWA6	Q91ZL0	091265	Q8NHW4	Q14745	Q9I8E0	080G56	
DB	9	φ	w	9	13	w	9	y	9	13	11	11	4	4	13	13	
* Query Match Length DB	91	91	91	92	91	50	93	92	92	06	92	92	92	80	89	91	
* Query Match	98.1	84.9	77.4	75.8	59.5	59.2	56.2	52.7	52.6	52.0	51.8	48.5	48.2	44.6	44.6	42.7	
Score	469	406	370	362.5	284.5	283	268.5	252	251.5	248.5	247.5	232	230.5	213	213	204	
ult No.	7	(1	٣	4	ហ	9	۲	œ	σ	10	11	12	13	14	15	16	

Q8hyn4 macaca mula Q8hyp9 macaca mula Q9quu2 mus musculu Q8m176 bos tatus norv Q9quu1 ratus norv Q9quu1 ratus norv Q9tu4 equus cabal Q9ttq4 equus cabal Q9ttq4 equus cabal Q9sm17 macaca mula Q8cm5 sigmodon hi Q8cm7 macaca mula Q8cm6 sigmodon hi Q8cm7 macaca mula Q8cm6 sigmodon hi Q8cm7 macaca mula Q8cm6 equus cabal Q9ttq3 equus cabal Q9cm6 equus cabal Q9fm1 macaca mula Q9cm6 equus cabal Q9fm1 equus cabal	Q81im4 paralichthy Q81im4 paralichthy Q81is7 guinea pig Q9ubg2 homo sapten Q8hyp7 macaca mula Q8hyp9 macaca mula Q8ayb2 ictalurus p Q8ayb7 rattus norv
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ALIGNMENTS

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RESULT 1 OBHYO1 ID OBHYO1 OBHYO1 DA (1) OBHYO1 OBHYO1 OBHYO1 OL-MAR-2003 (TEMBLrel. 23, Created) DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update) DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update) DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update) DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update) DE Chemokine CCL5/RAYTES. OS Macaca mulatta (Rhesus macaque). SE Unercyota; Metazoa; Chrordata; Craniata; Vertebrata; Buteleostomi; OC Enveryota; Macaca. ON CBL TaxID=9544; RA Basus Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.; RA Basus Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.; RT "Comprehensive cloning and sequencing reveals evolutionary CONSERVATION among all groups of knesus macaque chemokines."; RT "Conservation among all groups of knesus macaque chemokines."; RT Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE SHAN76072.1; SEQUENCE 91 AA; 10019 MW; BCBD69ED0573803B CRC64;	Query Match 98.1%; Score 469; DB 6; Length 91; Best Local Similarity 96.7%; Pred. No. 1.7e-47; Matches 88; Conservative 3; Mismatches 0; Indels 0; Gaps	1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYJARPLPRAHIKBYFYTSGKCSNP 60 	61 AVVFVTRKNRQVCANPEKKMVREYINSLEMS 91
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PRT;

PRELIMINARY;

RESULT 2
Q8MKD0
ID Q8MKD0
AC Q8MKD0;

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2 MTAVAVSLSILLVA-ALFPQASSSFFGADTTVCCFNYSVRKLPQNHVKDYFYTSSKCPQA 60
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57.8%; Pred. No. 7.9e-26;
iive 15; Mismatches 22; Indels 1; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21655115; PubMed=11797102;
Widthes S., Haynes A., O'Regan M., Bumstead N.;
"Identification, mapping, and phylogenetic analysis of three novel
chicken CC chemokines.";
                                                                                  Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.8%; Score 362.5; DB 6; Length 92; 72.8%; Pred. No. 5.5e-35; ive 10; Mismatches 14; Indels 1
                                                                                                                                                                                          SEQUENCE FROM N.A.

Kimura T., Kano R., Hasegawa A.;

Wimolecular cloning of feline RANTES gene.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB083479; BAB88940.1;
                                                                                                                                                                                                                                                                                             InterPro; IPR000827; CC chemkine sml.
InterPro; IPR001811; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
SMART; SM00199; SCY; 1.
SEQUENCE 92 AA; 10167 MW; 2E6F087140BA3CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       744A64BB229194EF CRC64;
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Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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SEQUENCE 91 AA; 10154 MW; 744A64BB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 53:674-683 (2001).
EMBL; AY037859; AAK84432.1; -
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IE8.
Pfam; PF00048; IL8; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Conservative
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                                                                                                                                                NCBI_TaxID=9685;
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                                                RANTES protein.
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Best Local 9
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Small inducible cytokine A5 RANTES.
Equus caballus (Horse).
Ebwarca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Perissodactyla, Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match B4.9%; Score 406; DB 6; Length 91; Local Similarity 83.5%; Pred. No. 4.2e-40; es 76; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 370; DB 6; Length 91;
Pred. No. 7.1e-36;
8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
                                                                                                                                                                                                                 Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D., "Eguus caballus RANTES mRNA.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enomoto A., Kano R., Hasegawa A.;
Enomoto A., Kano R., Hasegawa A.;
"molecular cloning of canine RAWIES gene.";
submitred (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB098662; BAC53725.1; -.
SEQUENCE 91 AA, 10179 MW; 01D79538CB8148E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00199; SCY; 1.
PROSITE; PS0047; SMAL CYTOKINES CC; 1.
SEQUENCE 91 AA: 10159 WW; AEBZ5328CD4ED7FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) RANTES protein.
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InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
Pfam: PF00048; ILB; 1.
SMART; SM00199; SCY; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
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Best Local Si
Matches 69,
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QBHYSO SULT 3

08SQ40 Q8SQ40;

SSULT 4 35040

1; Gaps

Query Match

m

Q8HYN5

IULT 6

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1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKVSAARLAVILIATALCAPASASPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                          Chemokine CCL3/MIP-1ALPHA.
Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A., "Comprehensive cloning and sequencing reveals evolutionary conservation among all groups of rhesus macaque chemokines.", Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF49267; AAN76071.1; - SEQUENCE 92 AA; 10103 MW; 80B2C2071565F809 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comprehensive cloning and sequencing reveals evolutionary conservation among all groups of rhesus macaque chemokines."; Submitted (Nov-2010) to the EMBL/GenBank/DDBJ databases. EMBL, AF49266; AANTGOTO.1; . CECUENCE 92 AA, 10119 MW; 021CAA371143D12A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 52.6*; Score 251.5; DB 6; Length 92;
l Similarity 47.8*; Pred. No. 6e-22;
44; Conservative 22; Mismatches 25; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.7%; Score 252; DB 6; Length 92; llarity 50.0%; Pred. No. 5.2e-22; Conservative 24; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TEMBLrel. 23, Last annotation update)
ChemoXine CCL4/MIP-18ETA.
                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 PGVIFLTKRGRQVCADPSKEWVQKYVSDLELS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PAVVFQTKRGKQVCADPSETWVQEYVNDLELN 92
61 PGVIFQTKKGRQVCANPTEDWVQEYITDLELN 92
                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                           Q8HYQ3
                                                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Hofmann-Lehmann R., Williams A.L., Swenerton R.K., Li P.-L.,
Rasmussen R.A., Chenine A.-L., McClure H.M., Kuprecht R.M.;
"Quantification of Simian Cytokine and Beta-Chemokine mRNAs using
Real-Time Reverse-Transcriptuse Polymerase Chain Reaction: Variations
in Expression during Chronic Primate Lentivirus Infection. ",
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammaila; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos. NCBI TaxID=9913;
                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 PCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.2%; Score 268.5; DB 6; Length 93; 53.3%; Pred. No. 6.1e-24; Live 18; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 59.2%; Score 283; DB 6; Length 50; Local Similarity 100.0%; Pred. No. 6.3e-26; les 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mentains C., and the modern of the continual of chemokines in RSV infection.", Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AN077840; AAL78060.1; --
InterPro; IPR00827; CC_chemkine sml.
InterPro; IPR011; Chemokine_IL®.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00048; IL8; 1. SMAET; SM00199; SCY; 1. SPROSTIE; PS00472; SMAEL CYTOKINES CC; 1. SEQUENCE: 93 AA; 10118 MW; 1266BFBFCEESEBE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 AA; 5789 MW; F58463F73E7E900B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JCT-2002 (TrEMBLrel. 22, Last annotation update)
Macrophage inflammatory protein-1 alpha.
Bos taurus (Bovine)
                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
RANTES (Fragment)
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 AA
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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OBSOA6

ULT 7

SEQUENCE nery Match

latches

2; Gaps

1,

1; Gaps

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Werling D.;

wery Match

latches

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1 MKVSAARLAVILIATALCAPASASPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKVPTAVLAVLLCITILCUQVESAPYGADTPTFCCESY-GRQIPRKFIADYFQTSSLCSE 59
                              1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                             Sigmodon hispidus (Hispid cotton rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Nubbs R.J., Barcellos L.F., Townson J.R.;

Nariation in gene copy number of the human chemokines macrophage inflammatory protein-la/CCL3 and macrophage inflammatory protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blanco J.C., Pleneva L.M., Prince G.A.;

"Sigmodon hispidus cyrckines, chemckines and interferons.";

"Sigmodon hispidus cyrckines, chemckines and interferons.";

Sigmodon hispidus cyrckines, chemckines and interferons.";

BNBL, ANGS407; AAL26704.1;

HSSP, Q9Y288; 1G28.

InterPro; IPR000827; CC_chemkine_sml.

InterPro; IPR001811; chemckine_ILB.

Fram; PF00448; ILB: 1.

SMART; SMO0199; SCV; 1.

SEQUENCE 92 AA; 10334 MW; CF9AAB3D94DCAF79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.5%; Score 232; DB 11; Length 92; 47.8%; Pred. No. 1.2e-19; tive 18; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1b/CCL4.";
Submirts AY079147; AAL87008.1; -.
InterPro; IPR000827; CC_chemkine_sml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein-1b2.
                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein-1 alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 PAVVEVTRKNROVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PGIIFLTKRNRHVCADPKETWVQEIITDLELN 91
                                                                                                 60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                           61 PAVVFLTRKCKEVCADPSQPWVNEYVNDLELN 92
                                                                                                                                                                                                                                                           92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=42415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                              RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.0%; Score 248.5; DB 13; Length 90; 50.0%; Pred. No. 1.3e-21; tive 20; Mismatches 23; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                  Hughes S.M., Bumstead N., "Mapping of the mammalian "Mapping of the gene encoding the chicken homologue of the mammalian chemokine SCYA4."
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.8%; Score 247.5; DB 11; Length 92; 46.7%; Pred. No. 1.8e-21; tive 21; Mismatches 27; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blanco J.C., Pletneva L.M., Prince G.A.; "Sigmodon hispidus cytokines, chemokines and interferons."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00199; SCY; 1.
PROSTITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 92 AA; 10195 MW, A34FDE21E6FA9C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF146730; AAD48772.1; -...
HSSP; P13236; 1HVM;
InterPro; IPRO10821; CC_chemkine_sml.
InterPro; IPRO10811; Chemokine_ILB.
Pfam; PF00448; ILB; 1.
SMART; SM00199; SCY; I.
SEQUENCE 90 AA; 9986 MW; 50AF9679A2675ICB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
C1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein 1 beta.
                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 AGVVFITRKGREVCANPONDWVQDYMNKMELN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sigmodon hispidus (Hispid cotton rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF421392, AAL16933.1; --
HSSP, Q9Y258, 1G28.
INCAPEO' IPRO00837; CC Chemkine sml.
InterPro; IPRO01811; Chemokine 1L8.
                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                          PRELIMINARY;
                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
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                                                                                                                                                       Chemokine.
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                                          O9PWA6
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ULT 10
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Job time : 31.3333 secs
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48.2%; Score 230.5; DB 4; Length 92;
Best Local Similarity 44.6%; Pred. No. 1.8e-19;
Matches 41; Conservative 22; Mismatches 28; Indels 1; Gaps 1;
                                                                                                                                                                                                                                                                                                           8 LAVILLATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LAVLLCTMALCNQFSASLAADTPTACCFSYTSRQIPQNFWADYFETSSQCSKPSVIFLTK 61
                                                                                                                                                                                                                                                                          1 MKVSAARLAVILIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
Ishlauka K., Igata-Yi R., Naruse K., Nakashima H., Ohuchi K.,
Kateuragi S., Kin Y., Ohmoto Y., Nomiyama H., Iio M., Miura R.,
Miyakawa T.;
Submitred (Aug.1995) to the EMBL/GenBank/DDBJ databases.
EMBL; D63785; BAA09855.1; --
HSSP; P13236; IHUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 44.6%; Score 213; DB 4; Length 80; Local Similarity 45.6%; Pred. No. 1.7e-17; es 36; Conservative 21; Mismatches 22; Indels
InterPro; IPR001811; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
SMART; SM00199; SCY; 1.
PROSTIE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 92 AA; 10166 MW; 4C9D01E926CDE882 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 80
80 AA; 8857 MW; 8B509EB15648E971 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Chemokine K203 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
1-MAR-2002 (TYEMBLrel. 20, Last annotation update)
LD78 alpha beta precursor (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
LD78 ALPHA BETA.
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                                                                                                                                                                                                                                                                                                                                                                                                                         61 PAVVFQTKRGKQVCADPSESWVQEYVYDLELN 92
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InterPro; IPR001811; Chemokine IE8.
Pfam; PF00048; IL8; 1.
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SEQUENCE
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CN K203

CN K2010

CN K2010

CN CALCADSARLIA; Chordata, Craniata; Vertebrata; Euteleostomi;

CN CALCADSARLIA; Avee; Neognathae; Galliformee; Phasianidae; Phasianinae;

CN CALLUB.

CN CAL
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Amino acid sequenc
Human chemokine RA
Novel human secret
Human EST encoded
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Wild type RANTES p
Wild type RANTES p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapi
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                                                                                                                                           December 16, 2003, 15:36:19; Search time 36.3005 Seconds (without alignments) 397.904 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SIDSI/ggddata/geneseq/geneseqp_emb1/AA1989.DAT:
| SIDSI/ggddata/geneseq/geneseqp_emb1/AA1990.DAT:
| SIDSI/gcgdata/geneseq/geneseqp_emb1/AA1990.DAT:
| SIDSI/gcgdata/geneseqfgeneseqp_emb1/AA1991.DAT:
| SIDSI/gcgdata/geneseqfgeneseqp_emb1/AA1993.DAT:
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| SIDS1/gcgdata/geneseqgeneseqp-emb1/AA1981.DAT: |
| SIDS1/gcgdata/geneseqgeneseqp-emb1/AA1981.DAT: |
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 protein - protein search, using sw model
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AAR97665
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AAY07231
AAY06727
AAB15790
AAU31766
AAM24003
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imum DB seq length: 2000000000
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Match Length DB
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20,000	Protein of K78A-RA Protein of R82A-RA Human SISD protein Protein of triple Protein of triple	4 2 2 2 2 2 2	rantes a RANTES p acid seq S chemokin chemokin RANTES p ANTES.	E Parago
ABB80929 AA021079 AAM52443 AA021086 AA021087	222	AANS2444 AAMS2444 AAW29538 AAY06728 AAY06760 AAW99707	AAY88331 AAY83898 AAO21100 AAO21100 AAO14140 AAR97666	AAR87668 AAR61765 AAB22134 AA020396 AA020396 AA020400 AA020401 AAU99754
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ALIGNMENTS

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RANTES; T-cell; T-lymphocyte; heparaname; heparin; heparan sulfate; arthritis; restenosis; cancer; wound healing.
AAR70802 standard; Protein; 91 AA
                                                                                                                                                      94WO-US08207.
                                                                                                                                                                              93US-0136117.
                                                                                                                                                                      93US-0099866
                                                                                                                                                                                                              Hoogwerf AJ, Ledbetter SR;
                                (updated)
(first entry)
                                                                                                                                                                                                                               WPI; 1995-082239/11.
N-PSDB; AAQ85372.
                                                                                                                                                                                             (UPJO ) UPJOHN CO.
                                                          RANTES protein.
                                                                                                                                                      26-JUL-1994;
                                                                                                                                                                    29-JUL-1993;
                                                                                                     Homo sapiens.
                                                                                                                                                                              13-OCT-1993;
                                                                                                                    WO9504158-A1
                                25-MAR-2003
29-AUG-1995
                                                                                                                                    09-FEB-1995.
                 AAR70802;
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0

100.0%; Score 478; DB 16; Length 91; 100.0%; Pred. No. 3.1e-46; ive 0; Mismatches 0; Indels (

91; Conservative

latches

wery Match lest Local Similarity

91 AA;

Seguence

AAR97665 standard; Protein; 91 AA

ULT 2 197665 14-FEB-1997 (first entry)

AAR97665;

inflammation; chemotaxis.

Homo sapiens

Key Peptide Protein

Claim 13; Page 51; 60pp; English

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This sequence represents the C-C chemokine RANTES. The invention relates antagonistic activity. The truncated chemokines are specifically residues is activity. The truncated chemokines are specifically residues 26 to 91 of the RANTES sequence (this sequence) or residues 29 to 99 of the MCP2 sequence (see AAY05300). The new chemokines are useful as medicaments, for diagnosis and/or treatment of diseases which require antagonistic activity of a chemokine e.g. inflammatory diseases. HIV infection, tumours, and anajogenesis—and haematopoiesis—related diseases. The invention also relates to the use of CD26/DPP IV for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-C chemokine; RANTES; MCP2; chemokine antagonist; inflammatory disease; HIV infection; tumour; angiogenesis-related disease; autoimmune disease; haematopoiesis-related disease; CD26/DPP IV; immune disease; diagnosis; atherosclerosis; pulmonary disease; skin disorder; therapy.
       This sequence represents full length human RANTES (Raised on Activation, normal T cell derived and Secreted). The DNA encoding this sequence was cloned from a human bone marrow lambda gill cDNA library using the primer sequences given in AAT30330-33. RANTES was used in the design of peptides which act as antagonists to RANTES or to MIP-lalpha (see also AAR97666-68). These peptides may be used in the treatment of asthma, allergic rhinitis, atopic dermatitis, atheroma/atheroscierosis or rheumatoid arthritis by inhibiting or reducing inflammation mediated by RANTES or MIP-lalpha. They are also useful in studying RANTES induced chemotaxis, mobilisation of Ca2+ and receptor binding.
                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity, for treatment of immune, inflammatory and infectious
                                                                                                                                                                                                                                                                                                                                   Length 91;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                              100.0%; Score 478; DB 17;
100.0%; Pred. No. 3.1e-46;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY05299 standard; protein; 91 AA
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-C chemokine, RANTES.
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                                                                                                                                                                                                                                                                                       91 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1997;
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                                                                                                                                                                                                                                                                                            Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, RANTES; Raised on Activation, normal T cell derived and Secreted; bone marrow; antagonist; MIP-lalpha, asthma; allergic rhinitis; atopic dermatitis; atheroma; atherosclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKVSAARLAVILIATALCAPASASPYSSDITPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                         Purified heparanases, prepared under reducing conditions and activated with transglutaminase, are given in AAR70786-802. Most are prepared by reverse transcription of mRNA from activated human leukocytes, then cloning of the cDNA into pVL1392 baculovirus vector, and expression in Sf9 cells in the presence of reduced glutathione and dithiothreitol.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide functioning as antagonist to RANTES or to MIP-1-alpha used in the treatment of e.g. asthma, allergic rhinitis, atheroma/atherosclerosis or rheumatoid arthritis
Screening for cpds. with anti-heparanase activity - by detecting inhibition of heparin or heparan sulphate degradation, potentially useful for treating arthritis, restenosis, cancer.
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/note= "RANTES, claim 3" /note= "Signal peptide" Location/Qualifiers

95WO-GB02861.

07-DEC-1995; 16-JUN-1995; 08-DEC-1994;

13-JUN-1996.

WO9617935-A2

94GB-0024835 95GB-0012319

Proudfoot AEI, Wells TNC;

WPI; 1996-287180/29.

N-PSDB; AAT30329.

(GLAX) GLAXO GROUP LTD.

Example; Fig 1; 33pp; English.

disorders.

Sequence Query Match

SULT 4

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This sequence represents the wild type C-C chemokine Regulated on Activation Normal T-cell Expressed and Secreted (RANTES). The invention relates the generation of amino-terminal truncated C-C chemokines, having chemokine antagonistic activity. The new chemokines are useful as an endicaments, for diagnosis and/or treatment of diseases which require antagonistic activity of a chemokine e.g. inflammatory diseases. HIV infection, tumours, and angiogenesis- and hematopoiesis-related diseases, including auto-immune diseases, atherosclerosis, pulmonary diseases and skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wild type, C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV; regulated on activation normal T-cell expressed and secreted; RANTES; truncation; antagonist, medicaments; diagnosis; inflammation; infection; tumour; anglogenesis; hematopoissis; autoimmune disease; atherosclerosis; pulmonary disease; skin disorder.
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                     1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                 1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New amino-terminally truncated C-C chemokines have antagonistic activity for treatment of immune, inflammatory and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 478; DB 20; Length 91; 100.0%; Pred. No. 3.1e-46; ive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                              61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                          AAY07231 standard; protein; 91 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wild type RANTES protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proost P, Struyf S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wild type; C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV; regulated on activation normal T-cell expressed and secreted; RANTES; truncation; antagonist; medicaments; diagnosis; inflammation; infection; tumour; angiogenesis; hematopolesis; autoimmune disease; atherosclerosis;
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                                                                                                                                                                                                                                                                                                        1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                         1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP
treatment of inflammatory, immune and infectious diseases, including
                        autoimmune diseases, atherosclerosis, pulmonary diseases and skin
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100.0%; Score 478; DB 20; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                      DB 20; Length 91;
                                                                                                                                                 100.0%; Score 478; DB 20;
100.0%; Pred. No. 3.1e-46;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY07235 standard; protein; 91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 1; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pulmonary disease; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98EP-0104216.
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                                                                                                                                                                                                        91; Conservative
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                                                                                                                                                                               Local Similarity
                                                                                                        91 AA;
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Proost P,

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Seguence

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The invention relates to a cross-over protein produced by chemical ligation of at least two functional protein modules derived from at least two functional protein modules derived from at least two parent protein molecules. The cross-over proteins can be used in pharmaceutical compositions for therapy of inflammatory and infectious diseases including AIDS, and for indications of hematopoiesis and chemoprotection. They are also useful for treatment of asthma, allergic chemoprising a collection of cross-over proteins is useful for screening for cross-over proteins that are receptor ligands. The libraries comprise for cross-over proteins that are receptor ligands. The libraries comprise functionally diverse compounds therefore improving the drug discovery process. The proteins and libraries are exemplified by the preparation of cross-over chemokines comprising various combinations of peptide cegments derived from RANTES, SDF-1 (stromal cell derived factor 1), VMIP (viral Macrophage Inflammatory protein) and other such chemokines. The present sequence represents a native amino acid fragment of RANTES.
                                                                                                                                                                                                                                                                                                                                                                                    Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral; infectious disease; hematopoiesis; chemoprotecthon; atthma; RAPTES; wMIP; allergic rhintis; arcpic dermatitis; rheumatoid arthritis; SDF-1; MPAV; stromal cell derived factor 1; Macrophage Inflammatory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cross-over proteins for treatment of inflammation and infections e.g. AIDS - prepared by ligation of two functional protein modules derived from two different parent molecules
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                                                                                                                                                                                                                                                                                                               Amino acid sequence of native RANTES.
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                                                                        AAY06727 standard; protein; 91 AA
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Les 91, Conservative
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SSULT 6
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                                                                                    Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis; monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV; AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia; basophil-mediated disease; myocardial infarction; acute ischaemia; rheumatoid arthritis; contraception.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention concerns the identification of a number of chemokines which can be used to produce derivatives, agonists and antagonists which are then useful in disease treatment. The chemokines include sequences AAB15794, AAB15803-B15813 and AAB1581-B15848. These chemokine derivatives can be used to treat diseases such as autoimmune diseases, antherosclerosis, osteoporosis, HV infection and AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated diseases, endotoxaemia, myocardial infarction, acute ischaemia and themmatoid arthritis, and can be used to prevent strokes and as contraceptives. The coding sequences for the chemokines can be used in gene therapy for the same diseases, as well as in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and for treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 478; DB 21; Length 91; 100.0%; Pred. No. 3.1e-46; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                  Human chemokine RANTES SEQ ID NO: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 134; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU31766 standard; Protein; 445 AA.
                                                                                                                                                                                                                                                                                                                     12-JAN-2000; 2000WO-US00821.
                                                                                                                                                                                                                                                                                                                                                           99US-0229071.
                                                                                                                                                                                                                                                                                                                                                                       99US-0271192
99US-0452406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tatalick LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2001 (first entry)
              17-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-499101/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA74884
                                                                                                                                                                                                                                            WO200042071-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animal models.
                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              17-MAR-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grainger DJ,
                                                                                                                                                                                                                                                                                                                                                           12-JAN-1999;
                                                                                                                                                                                                                                                                                 20-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU31766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AAU31766
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WO200179449-A2. Homo sapiens.

25-OCT-2001

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ABB80929 standard; Protein; 91 AA
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                                                                                                                                                                                                                          25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                       25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-476164/51.
                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAH98662.
                                                                                                    WO200154477-A2.
                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                            02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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  임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically mincrease to express them are also useful for producing the proteins. The proteins are useful in genetic one succination, testing and therapy, and can be used as nutritional supplements. They may be used to have a stem cell proliferation, to regulate hammatopoiesis; and in the contents of the polyperior and the contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAXIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                            stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, sheep, pig, cow, fruit fly, yeast, hamster, macaque, horse, tomato, monkey, dog, sea urchin, expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 478; DB 22; Length 445; 100.0%; Pred. No. 1.9e-45;
                                        Human, vaccination; gene therapy, nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 100.0%; Pred. No. 1.9991; Conservative 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human EST encoded protein SEQ ID NO: 1528.
Novel human secreted protein #2257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 506; 765pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM24003 standard; Protein; 91 AA
                                                                                                                                                                                                                                                                                                                                                                                               Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                 16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                       18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
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Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 AA;
                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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Seguence

latches

AAM24003;

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forematics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paramyxovirus; infection; RANTES; chemokine; antiviral; CCR1; CCR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "specifically claimed mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 12; DB 22; Length 91; Local Similarity 98.9%; Pred. No. 1.5e-45; Local Similarity 98.9%; Pred. No. 1.5e-45; Indels 1; Indels
diagnostics, forensic test, gene mapping, genetic disorder, biodiversity, gene therapy, nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YI, Liu C, Zhou P, Qian XB, Wang Z, Chen R,
Cao Y, Drmanac RA, Zhang J, Werhman T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 1053; 1275pp; English.
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WO200255019-A2.

18-JUL-2002

Holtzman MJ;

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chemokine mutant), comprising the amino sequence of 91 amino acids as given in the specification. The CC chemokine mutant RANTES, with two mutations in the cationic site is useful for the preparation of a pharmaceutical composition used in treating multiple sclerosis or other demyelinating diseases. The mutant with single mutations at cationic sites is used for the treatment of HIV infection and/or other allergic or inflammatory disease. This sequence represents the wild-type human RANTES protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKVSAAALAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP
                                                                                                                                    A mutant of the human CC chemokine RANTES with two mutations in the cationic site of the 40^{\circ}s loop is used for treatment of multiple sclerosis and/or demyelinating diseases -
                                                                                                                                                                                                                                                                                                                          The invention relates to a truncated and mutated human RANTES (a CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 98.7%; Score 472; DB 23; Length 91; Local Similarity 98.9%; Pred. No. 1.5e-45; nes 90; Conservative 0; Mismatches 1; Indels
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                Proudfoot A, Wells TNC, Kosco-Vilbois M;
                                                                                                                                                                                                                                                                  Examples; Page 36; 46pp; English.
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                                                                                WPI; 2002-340073/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6303295-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the treatment of paramyxovirus infection that involves administration of an active ingredient such as RANTES chemokine (I) or an expression system (II). (I) and (II) are used in the treatment and diagnosis of paramyxovirul infection, especially in children. RANTES chemokine has a significant effect on respiratory infections caused by paramyxovirus. RANTES acts downstream of vixal entry and signals through specific CCII and/or CCR5 chemokine receptors to interrupt the death pathway of macrophages which have been infected by virus. RANTES not only inhibits apoptosis of infected macrophage but also clears the macrophage of infection. The present sequence represents a human RANTES protein. Note: the present sequence is not provided in the specification. It has been obtained from the NCBI database under the accession no. NP_002976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of RANTES chemokine or an expression system in treatment and diagnosis of paramyxovirus infection, especially in children -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.7%; Score 472; DB 23; Length 91; 98.9%; Pred. No. 1.5e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page -; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.9%;
Matches 90; Conservative
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                                                                                                                                                 23-OCT-2001; 2001WO-US45244.
                                                                                                                                                                                                           24-OCT-2000; 2000US-243264P.
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                                                                                                                                                                                                                                                                      (UNIW ) UNIV WASHINGTON.
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Sequence

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The present invention relates to selenoproteins encoded in the genome of a virus, where the coding sequence of the selenoprotein is genetically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nadimpalli RG, Ramanathan CS;
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AAM52443 standard; Protein; 91 AA
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                                                                                                                                                                                                                                                                                                                                                          HIV Nef1 fusion protein #10.
                                                                                                                       CCC X S X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

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engineered for expression in a nucleic acid construct. The invention also discloses a method for identifying selenoprotein coding sequences, for detecting certain viruses (e.g. HIV or Ebola), cancer and immune system disorders. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human; chemokine mutant; cationic site; multiple sclerosis; HIV infection; inflammatory disease; demyelinating disease; allergic; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemokine mutant), comprising the amino sequence of 91 amino acids as given in the specification. The CC chemokine mutant RANTES, with two mutations in the cationic site is useful for the preparation of a pharmaceutical composition used in treating multiple sclerosis or other demyelinating diseases. The mutant with single mutations at cationic sites is used for the treatment of HIV infection and/or other allergic or inflammatory diseases. This sequence represents a mutant human RANTES protein of the invention.
                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                            1 MKVSAAALAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                    1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP
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                                                                                                                                                                                                                      Length 91;
                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                            98.7%; Score 472; DB 23;
98.9%; Pred. No. 1.5e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AVVEVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO21086 standard; Protein; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein of R44A-RANTES mutant.
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                                                                                                                                                                                                                                                                          Conservative
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Matches 89; Conservative
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                                                                                                                                                                                                                                             Similarity
                                                                                                                                                        91 AA;
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Best Local
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                                                                                                                                                                                                                                                                                                                                RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human; chemokine mutant; cationic site; multiple sclerosis; HIV infection; inflammatory disease; demyelinating disease; allergic; mutein.
                    1 MKVSAAALAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                   91
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                                                                   61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS
                                                                                                 61 AVVEVTAKNROVCANPEKKWVREYINSLEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Examples; Page 39; 46pp; English.
                                                                                                                                                                                           AAO21087 standard; Protein; 91
                                                                                                                                                                                                                                                                                                Protein of K68A-RANTES mutant.
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The invention relates to a truncated and mutated human RANTES (a CC chemokine mutant), comprising the amino sequence of 91 amino acids as given in the specification. The CC chemokine mutant RANTES, with two mutations in the cationic site is useful for the preparation of a pharmaceutical composition used in treating multiple sclerosis or other demyelinating diseases. The mutant with single mutations at cationic sites is used for the treatment of HIV infection and/or other allergic or inflammatory diseases. This sequence represents a mutant human RANTES protein of the invention.
                                                                                                                                                                                                                                                                                                                                     RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human; chemokine mutant; cationic site; multiple sclerosis; HIV infection; inflammatory disease; demyelinating disease; allergic; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A mutant of the human CC chemokine RANTES with two mutations in the cationic site of the 40's loop is used for treatment of multiple sclerosis and/or demyelinating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Arg substituted by Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
Misc-difference 70
                                                               AA021088 standard; Protein; 91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; Page 40; 46pp; English.
                                                                                                                                                                                                                                                                     Protein of R70A-RANTES mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-2001; 2001WO-EP11428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2000; 2000EP-0121665.
                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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Search completed: December 16, 2003, 15:37:49
Job time : 37.3005 secs

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Query Match

97.5%; Score 466; DB 23; Length 91;
Best Local Similarity 97.8%; Pred. No. 6.9e-45;
Matches 89; Conservative 0; Mismatches 2; Indels

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Sequence 29, Appli
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Sequence 8, Appli
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Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 11, Appli
Sequence 29, Appli
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Sequence 29, Appli
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Sequence 9, Appli
                                                                      December 16, 2003, 15:39:40; Search time 24.3661 Seconds (without alignments) 694.592 Million cell updates/sec
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                                                                                                                                   478
1 MKVSAARLAVILIATALCAP......VCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-920-1374-29
US-09-920-1374-29
US-09-537-658-1
US-10-137-65-8
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US-09-144-838-42
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US-09-144-838-9
US-09-834-795A-29
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Sequence 32, Appl
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Sequence 32, Appli
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330, App
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Sequence 36,
Sequence 39,
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Sequence 2,
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9 US-09-144-838-46
10 US-09-537-888-2
10 US-09-1844-838-5
9 US-09-144-838-40
9 US-09-144-838-40
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9 US-09-144-838-44
10S-09-144-838-39
10S-10-223-085-33
10S-10-223-085-33
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10S-10-223-085-33
10S-10-223-088-33
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ALIGNMENTS

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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                 APPLICANT: Grainger, David J.
APPLICANT: Grainger, Lauen Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 295.022US1
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT APPLICATION NUMBER: US/08/927,939
NUMBER OF SEG ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                ; Sequence 21, Application US/08927939
; Publication No. US20010006640A1
; GENERAL INFORMATION:
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US-08-927-939-21
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RESULT 1
US-08-927-939-21
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US-09-144-838-9
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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APPLICANT: Siani, Michael A.
APPLICANT: Wilken, Jill
APPLICANT: Wilken, Jill
APPLICANT: Simon, Reyna
APPLICANT: Simon, Reyna
APPLICANT: Simon, Reyna
APPLICANT: Rent, Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
TITLE REPREBENCE: RREN-020/01US
CURRENT APPLICATION NUMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: US 60/057,620
BARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic -09-144-838-9
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100.0%; Score 478; DB 9; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.4e-47;
Matches 91; Conservative 0; Mismatches 0; Indels
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Sequence 29, Application US/09834795A
Sequence 29, Application US/09834795A
Sequence 29, Application:
GENERAL INCORMATION:
APPLICANT: Lawrence, Papsidero
APPLICANT: Lyn, Dyster
APPLICANT: Jana, Funstari
TITLE OF INVENTION: Detection and Treatment of Breast Cancer
FILE REFERENCE: 3380/11127-US3
CURRENT APPLICATION NUMBER: 2001-04-12
PRIOR APPLICATION NUMBER: 09/146,580
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PRIOR APPLICATION NUMBER: 60/071,899
PRIOR FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 60/092,155
PRIOR FILING DATE: 1998-07-09
NUMBER OF SEO ID NOS: 35
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Matches 91; Conserv
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SEQ ID NO 29
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61 AVVEVTRKNRQVCANPEKKWVREYINSLEMS 91

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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKBYFYTSGKCSNP 60
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  Sequence 29, Application US/09834794A

Sequence 29, Application US/09834794A

Sequence 29, Application US/09834794A

GENERAL INFORMATION:
APPLICANT: Lyn, Dyster
APPLICANT: Lyn, Dyster
APPLICANT: Jana, Frustaci
TITLE OF INVENTION: Detection and Treatment of Breast Cancer
FILE REFERENCE: 330/11127-US4

CURRENT PPLING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: 09/146,580

PRIOR FILING DATE: 1998-09-03

PRIOR FILING DATE: 1998-01-20

PRIOR FILING DATE: 1998-01-20

PRIOR FILING DATE: 1998-01-20

PRIOR FILING DATE: 1998-01-20

PRIOR FILING DATE: 1998-01-20
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Publication No. US20030049725A1
CENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Bandman, Olga
APPLICANT: Wilde, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AVVPVTRKNRQVCANPEKKWVREYINSLEMS 91
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/920,137A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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REGISTRATION NUMBER: 33
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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US-09-834-794A-29
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TOPOLOGY:
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Sequence 1, Application US/09537858
Publication No. US20030119148A1
Sequence 1. Normarion:
SPREALL INFORMATION:
APPLICANT: PROST, PAUL
APPLICANT: PROST,
APPLICANT: OF INVENTION:
APPLICANT: OF INVENTION: AMINO-TERMINALLY TRUNCATED RANTES AS CHEMOKINE
TITLE OF INVENTION: AMINO-TERMINALLY TRUNCATED RANTES AS CHEMOKINE
FILE REFERENCE: 2024/49674
CURRENT PELING DATE: 2010-02-26
NUMBER OF SEQ ID NOS: 2
SOFTWARENT FILING DATE: 2010-02-26
NUMBER PROFILE PARCELLING VEY: 2.1
                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 470; DB 11; Length 91; 100.0%; Pred. No. 6.4e-47; ative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                              Query Match 100.0%; Score 478; DB 11; Length 91; Sest Local Similarity 100.0%; Pred. No. 6.4e-47; Aatches 91; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10137655
Publication No. US20030138917A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Bandman, Olga
APPLICANT: Milde, Craig G.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 91, Conservative
                     single
                                                                   MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                      GenBank
amino acid
                                             linear
                                                                                                                   LIBRARY: Genba
                        STRANDEDNESS:
                                                                                                                                                                   -09-920-137A-8
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 478; DB 12; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.4e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/467,123B
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPRATING SYSTEM: DOS
COTWARE: FREESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/137,655
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: Genbank
                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
CA
U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: RANTES
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                              94304
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118-02-370-13/8-6.radd

1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60 1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60 Matches

Sequence 8, Application US/10057275
Publication No. US2020155545A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
Bandman, Olga
Wilde, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS NUMBER OF SEQUENCES: 11 -10-057-275-8

ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto CORRESPONDENCE ADDRESS:

U.S. ZIP: 94304 COUNTRY:

SOFTWARE: FastSEQ Version 1.5 COMPUTER: 1BM Compatible OPERATING SYSTEM: DOS COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/057,275
FILING DATE: 25-Jan-2002
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/390,740A FILING DATE: February 17, 1995 ATTORNEY/AGENT INFORMATION: NAME: Luther, Barbara J. REGISTRATION NUMBER: 33,954 REFERENCE/DOCKET NUMBER: PF-0027 US

TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-852-0195 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids STRANDEDNESS: single TYPE: amino acid

1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60 0; Gaps . Match 100.0%; Score 478; DB 14; Length 91; Local Similarity 100.0%; Pred. No. 6.4e-47; les 91; Conservative 0; Mismatches 0; Indels (61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91 61 AVVFVTRKARQVCANPEKKWVREYINSLEMS 91 SEQUENCE DESCRIPTION: SEQ ID NO: 8: MOLECULE TYPE: peptide IMMEDIATE SOURCE: LIBRARY: GenBank CLONE: RANTES US-10-057-275-8 Query Match ò

APPLICANT: Wilde, Craig G.
APPLICANT: Walde, Craig G.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Scilhamar, Olga
APPLICANT: Scilhamar, Jeffrey J.
TITLE OF INVENTION: DNA ENCODING LIVER EXPRESSED CHEMOKINE
FILE REFERENCE: PF-0034-3 CON
CURRENT APPLICATION NUMBER: US/10/293,705
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/208,803
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 08/798,143
PRIOR FILING DATE: 1997-02-10
PRIOR APPLICATION NUMBER: 08/798,143
PRIOR FILING DATE: 1994-11-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL Program NAME/KEY: misc_feature OTHER INFORMATION: GenBank ID No. US20030083468A1 g134510 ; Sequence 12, Application US/10293705; Publication No. US20030083468A1; GENERAL INFORMATION: TYPE: PRT ORGANISM: Homo sapiens US-10-293-705-12 -10-293-705-12 SEQ ID NO 12 LENGTH: 91

1 MKVSAARLAVILIATALCAPASASPYSSOTTPCCFAYIARPIPRAHIKEYFYTSGKCSNP 60 1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91 ò q

0; Gaps

Query Match
100.0%; Score 478; DB 15; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.4e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0

Sequence 10, Application US/09144838A

Parent No. US20020051996A1

GENERAL INFORMATION:
APPLICANT: Siani, Michael A.
APPLICANT: Milken, Jill
APPLICANT: Siann, Reyna
APPLICANT: Siann, Reyna
APPLICANT: Siann, Reyna
APPLICANT: Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation RESULT 11 US-09-144-838-10

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24 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVRE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKKVRF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stant, Michael A.
APPLICANT: Stant, Michael A.
APPLICANT: Simon, Reyna
APPLICANT: Simon, Reyna
APPLICANT: Simon, Reyna
APPLICANT: Stant, Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
FILE REFERENCE: GREN-020/01US
CURRENT APPLICATION NUMBER: US 60/057,620
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER PAIGN DATE: 1997-09-04
SOFTWARE: PAIGN DAS: 54
SOFTWARE: PAIGN OF 1.
SEQ ID NOS: 54
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                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.2%; Score 374; DB 9; Length 68; Best Local Similarity 100.0%; Pred. No. 3.2e-35; Matches 68; Conservative 0; Mismatches 0; Indels
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FILE REFERENCE: GRFN-020/01US
CURRENT APPLICATION NUMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-144-838-42
Sequence 42, VDPD1ication US/09144838A
Patent No. US20020051996A1
GENERAL INFORMATION:
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Sequence 11, Application US/09195457
Patent No. US20020081623A1
GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Seguence
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                                                                                                                                                                                                                          SEC ID NO 10
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                                                                                                                                                                                                                                                                                         PRT
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APPLICANT: MCDOAAIG, John R.
APPLICANT: MCDOAAIG, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE A
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PATENTING VAT: 2.0
SEQ ID NO 29
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVRE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVRE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.2%; Score 374; DB 9; Length 68; 100.0%; Pred. No. 3.2e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match ... Best Local Similarity 100.0%; Pred. No. 3.40
           AFFLICANT: HSUAN, JOHN J.

TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
FILE REFERENCE: 550-33
CURRENT APPLICATION NUMBER: US/09/195,457
CURRENT FILING DATE: 1998-11-18
PRIOR PELING DATE: 1998-11-18
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1994-09-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 11
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-792-793A-29
Sequence 29, Application US/09792793A
Factor No. US20020168370A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 YINSLEMS 91
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US-10-375-209A-29
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GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: McDonald, John R.
TITLE COGGISS. PAILISP
TITLE OF INVENTION: MCTHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAWAGE AND TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601E
CURRENT APPLICATION UNDEER: US/10/375,209A
CURRENT PILLNG DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 93
SEQ THARE: PATENTIN VEY: 2.0
SEQ ID NO 29
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
78.2%; Score 374; DB 12; Length 68;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVRE 83
1 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVRE 60
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRI
ORGANISM: homo sapien
FEATURE:
OTHER INFORMATION: Human Chemokine Polypeptide: RANTES
-10-375-209A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YINSLEMS 68
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!arch completed: December 16, 2003, 15:48:25
!b time : 25.3661 secs

Sequence 8, Appli Sequence 5, Appli

Sequence

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Seguence

Sequence

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Sequence 36, Application PC/TUS9408207A
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Hoogewerf, Arlene J. and Ledbetter, Steven R.
TITLE OF INVENTION: USE OF HEPRARANSE TO IDENTIFY AND
TITLE OF INVENTION: ISOLATE ANTI-HEPRARANSE COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: The Upjohn Company, Intellectual Property Law 301 Henrietta
DCT-US94-08207-36

US-08-136-17-36

US-08-136-17-36

US-08-136-17-36

US-08-467-123-5

US-08-927-939-21

US-08-927-939-21

US-08-927-939-21

US-09-027-939-21

US-09-113-705-8

US-09-113-705-1

US-09-113-705-1

US-09-113-705-1

US-09-113-705-1

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US-08-479-620-21

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US-08-58-658-21

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US-08-58-68-21

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US-08-58-68-21

US-08-58-68-21

US-08-58-68-21

US-08-58-68-21

US-09-58-113-28

US-08-478-61-15-8

US-08-478-61-15-8

US-08-478-61-13-8

US-08-45-444-73-11

US-08-45-444-73-11
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08207A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalamazoo
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STREET: 30
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                                                                                                                                                                 Sequence 36, Appl
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500.045 Million cell updates/sec
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                                                                                                                                                            December 16, 2003, 15:37:55 ; Search time 165.59 Seconds
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/ cgn2 6/ptodata/1/paa/US06 COMB.pep: *
/ cgn2 6/ptodata/1/paa/US06 COMB.pep: *
/ cgn2 6/ptodata/1/paa/US06 COMB.pep: *
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/cgn2_6/ptodata/1/paa/US103_COMB.pep:*
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|/paa/US100_COMB.pep:+
|/paa/US100_COMB.pep:+
|/paa/US101_COMB.pep:+
|/paa/US102_COMB.pep:+
|/paa/US103_COMB.pep:+
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|/paa/US104_COMB.pep:+
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                                                     Compugen Ltd.
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compue
                                                                                                                                                                                                                                                                                                                                                                                                                                                cal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                      5728757 seqs, 909918778 residues
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                                                                                                                    protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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rfect score:
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Sequence 21, Appl Sequence 21, Appl Sequence 115540, Sequence 16, Appl Sequence 16,

5, Appli 1, Appli 1, Appli 1, Appli 22750, A

Appli

Sequence 8, Appli Sequence 8, Appli Sequence 5, Appli Sequence 12, Appl Sequence 8708, Ap Sequence 8708, Ap

Sequence 21, Appl

Sequence 21

Sequence

Sequence 2 Sequence 2

29, Appl

13789, A

289, App

Seguence

Sequence Sequence Sequence Sequence Sequence Sequence us-09-920-137a-8.rapm

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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: The Upjohn Company, Intellectual Property Law : 301 Henrietta
Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%; Score 478; DB 1; Length 91; Local Similarity 100.0%; Pred. No. 2.9e-46; les 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application PC/TUS9408207
GENERAL INFORMATION:
APPLICANT: Hoogewerf, Arlene J.
APPLICANT: Leabetter, Steven R.
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/08207
                                NAME: Jameson, William G.
REGISTRATION NUMBER: 27,199
REPERSONCE/DOCKET NUMBER: 4731.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/385-7561
TELEPHONE: 616/385-6897
                                                                                                                                 TELEFAX: 616/JUL
TELEX: 224401
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 27,199
REPERENCE/COCKET NUMBER: 473
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/385-7561
TELEPRAX: 616/385-6897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 224401
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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                  ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
TT-US94-08207-36
                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
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CLASSIFICATION:
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:T-US94-08207-36
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                 1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                               0; Gaps
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100.0%; Score 478; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s: The Upjohn Company, Intellectual Property Law 301 Henrietta
Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hoogewerf, Arlene J.
APPLICANT: Hoogewerf, Steven R.
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND
TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMFOUNDS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 27,199
REFERENCE/DOCKET NUMBER: 4731.1 CP
TELECOMMUNICATION INFORMATION:
TELEBHONE: 616/385-7561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 8, Application US/08390740B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                ; Sequence 36, Application US/08136117; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 616/385-689/
TELEX: 224401
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Jameson, William G.
REGISTRATION NUMBER: 27,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-390-740B-8
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APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,
TITLE OF INVENTION: ITS PRODUCTION AND USES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 478; DB 7; Length 91; 100.0%; Pred. No. 2.9e-46; tive 0; Mismatches 0; Indels
APPLICANT: Bandman, Olga
APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
TILE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: JAJURESS:
STREET: JAJO HILLVIEW AVENUE
CITY: PALO ALTO
COUNTY: CALIFORNIA
ZIP: QAI'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AVVEVTRKNROVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0027 US
                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,740B
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Luther, Bathara J.
REGISTRATION NUMBER: 33,954
REPERENCE/DOCKET NUMBER: PF-00
TELECOMMUNICATION INPORMATION:
TELEPAX: 415-855-055
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08467123 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                         IBM Compatible
SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91; Conservative
                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: GenBank
CLONE: RANTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COM
OPERATING SYSTEM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                 U.S.
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                               COUNTRY: U
ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -08-467-123-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENGTH:
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 478; DB 8; Length 91; Best Local Similarity 100.0%; Pred. No. 2.9e-46; Matches 91; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Grainger, David J.
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: Ompounds and methods to inhibit or
TITLE OF INVENTION: Ompounds and methods to inhibit or
CURRENT APPLICANTION: 1997-09-11
CURRENT FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 83
SOTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0026 US
TELECOMMUNICATION INFORMATION:
                     APPLICATION NUMBER: US/08/467,123
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                       (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 855-0572
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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US-08-927-939-21
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US-09-023-092-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 478; DB 13; Length 91; 100.0%; Pred. No. 2.9e-46; trive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09023092
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Zlounk, Albert
APPLICANT: Greene, Onicholas J.
APPLICANT: Greene, Jonathan R.
TITLE OF INVENTION: Mammalian Chemokines; Related Reagents
TITLE OF INVENTION: and Methods
                                                                                     APPLICANT: Crainger, David J.
APPLICANT: Tatalick, Lauren Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REPERENCE: 1543.001US1
CURRENT APPLICATION NUMBER: US/08/927,939A
CURRENT FILING DATE: 1997-11-09
NUMBER OF SEC ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,092
FILING DATE: 13-FEB-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2: DNAX Research Institute
901 California Avenue
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                                             Sequence 21, Application US/08927939A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650/32)
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
1*TANGTH; 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Rese
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Californía
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TWDF: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 91; Conserva
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       SULT 7
-08-927-939A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                           SEQ ID NO 21
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                                                                                            1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                            0; Gaps
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Query Match
100.0%; Score 478; DB 14; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09113705

GENERAL INFORMATION:
APPLICANT: BANDMAN, OLGA
APPLICANT: COLENAN, ROGER
APPLICANT: COLENAN, ROGER
APPLICANT: STUART, SUSAN G.
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
STREET: Palo Alto
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AVVEVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                   61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REGISTRATION NUMBER: 37954
REFERENCE/DOCKET NUMBER: PF-0031 US
TELECHONE: 415-85-055
ITELEPHONE: 415-85-0155
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144
FILING DATE: 13-APR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 91, Conserva
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TELECOMMUNICATION INFORMATION:
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Siani, Michael A.
APPLICANT: Siani, Michael A.
APPLICANT: Siani, Michael A.
APPLICANT: Siani, Reyna
APPLICANT: Siani, Reyna
APPLICANT: Siani, Reyna
APPLICANT: Siani, Reyna
APPLICANT: Remt, Stephan B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
TITLE OF INVENTION: Modular D.S.020/01US
CURRENT APPLICATION UNMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: US 60/057,620
BARLIER APPLICATION NUMBER: US 60/057,620
BARLIER OF FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 1947-08-08-04
SOFTWARE: PATENTIN Ver. 2.1
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100.0%; Score 478; DB 15; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels (
                                                                             APPLICANT: BADMEAN, Olga
APPLICANT: Coleman, Roger
APPLICANT: Coleman, Roger
APPLICANT: Stuart, Susan G.
TILLE OF INVENTION: NUMBER: US/09/113,705A
CURRENT APPLICATION NUMBER: US/09/113,705A
UNMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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     i-09-113-705-5
Sequence 5, Application US/09113705A
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Rantes
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-09-150-813-21
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3-09-144-838-9
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                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5
LENGTH: 91
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Local Similarity 100.0%; Score 478; DB 15; Length 91;
Lecal Similarity 100.0%; Pred. No. 2.9e-46;
Les 91; Conservative 0; Mismatcher
APPLICANT: Grainger, David J.
APPLICANT: Tatallok, Lauen Marie
APPLICANT: Tatallok, Lauen Marie
APPLICANT: Tatallok, Suzanne T.
TILE OF INVENTION: Compounds and methods to inhibit or
TILE OF INVENTION: augment an inflammatory response.
FILE REPRENENCE: 295.027031
FILE REPRENENCE: 295.027031
CURRENT APPLICATION NUMBER: US/09/150,813
CURRENT FILING DATE: 1998-09-11
SEALIER APPLICATION NUMBER: US 08/927939
EARLIER APPLICATION NUMBER: US 08/927939
SARLIER APPLICATION NUMBER: 105
SUFTARE: FasteSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHEMOKINES, THEIR
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GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES,
TITLE OF INVENTION: PRODUCTION AND USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/208,803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0024
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29-NOV-1994
JMBER: 08/303,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ Version 1.5
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APPLICATION NUMBER: 08/347,
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: 08/303,
FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-150-813-21
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US-09-208-803-12
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415-855-0555

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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Bandman, Olga
PPLICANT: Coleman, Roger
PPLICANT: Stuart, Sisan G
ITLE OF INVENTION: NEW CHEWOKINE EXPRESSED IN EOSINOFHILS
ITLE REFERENCE: PP-0031-2 DIV
URRENT APPLICATION NUMBER: US/09/360,290
URRENT FILING DATE: 1999-07-22
URRENT FILING DATE: 1995-04-13
ARLIER FILING DATE: 1995-04-13
ARLIER FILING DATE: 1995-04-13
ANDER OF SEQ ID NOS: 8
AUMBER OF SEQ ID NOS: 8
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APPLICANT: Wilde, Craig C.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,
TITLE OF INVENTION: ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 478; DB 16; Length 91; 1. Similarity 100.0%; Pred. No. 2.9e-46; 91; Conservative 0; Mismatches 0; Indels (
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Sequence 5, Application US/09387620
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: 415-855-0555
TELEPAX: 415-852-0195
ORMATION FOR SEQ ID NO: 12:
EQUENCE CHARACTERISTICS:
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09-360-290-5
                                                                                                                                             , 91 amino acids amino acid
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                           MMEDIATE SOURCE:
                                                                                                                                                                                                                                 single
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t Local Similarity
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                                                                                                                                                                                                                                                                                   TOPOLOGY:
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYLARPLPRAHIKEYFTSGKCSNP 60
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Job time : 165.59 secs
                                                                                                                                                                                                                                                                                                                                                                             PF-0026-1 DIV
         Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                     RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,123
                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FRAESEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,620
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PP.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-555-0555
TELEPHX: 415-845-4166
                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                               3174 Porter Drive
Palo Alto
                                                                                                                      COMPUTER REPABLE FORM:
COMPUTER TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                          USA
                                                                                                           94304
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                        ADDRESSEE:
                                                                                            COUNTRY:
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US-60-487-610-2474
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LENGTH: 91
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182.5
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Sequence 1666, Ap
Sequence 1666, Ap
Sequence 1677, Ap
Sequence 1051, Ap
Sequence 3, Appli
Sequence 9, Appli
Sequence 9, Appli
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Sequence 11, Appl
Sequence 13, Appl
Sequence 3, Appl
Sequence 6, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 2474, Ap
Sequence 1561, Ap
Sequence 8, Appli
Sequence 9, Appli
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366.280 Million cell updates/sec
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                                                                                                                                                                                  December 16, 2003, 15:38:25 ; Search time 13.4262 Seconds
                                                                                                                                                                                                                                                                                                                                                                     1 MKVSAARLAVILIATALCAP........VCANPEKKWVREYINSLEMS 91
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| cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/USIO_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/USIO_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/USIO_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-60-487-610-2474

US-60-488-450-1561

US-10-398-457-9

US-10-398-457-10

US-10-398-457-11

US-10-398-457-11

US-10-398-457-11

US-10-398-457-11

US-10-398-457-13

US-10-398-457-13

US-10-398-457-14

US-10-398-457-17

US-10-398-457-17

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US-10-398-457-17

US-10-398-457-1078

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US-60-485-450-1058

US-60-487-610-1666

US-60-487-610-1677

US-60-488-450-1051

US-60-488-450-1051
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       protein - protein search, using sw model
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Match Length
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US-10-398-457-1
; Sequence 1, Application US/10398457
; GENERAL INFORMATION:
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
; TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INPECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO1449
CURRENT APPLICATION NUMBER: US/60/487,610
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2474
                                             Sequence 5, Applil
Sequence 885, App
Sequence 930, App
Sequence 277, App
Sequence 279, App
Sequence 281, App
Sequence 2476, App
Sequence 476, App
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                                                                                                                                                                                                                       Sequence 15, Appl
Sequence 35, Appl
Sequence 41, Appl
Sequence 18, Appl
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                                                                                                                                                                         Sequence 2330, Ap
Sequence 4411, Ap
Sequence 2730, Ap
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                                   Sequence 10,
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                  Sequence
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Pred. No. 6.4e-46;
0; Mismatches 1; Indels
US-10-332-038A-8

US-10-398-457-31

US-10-398-457-31

US-10-398-457-10

US-10-398-457-5

PCT-US03-28745-885

PCT-US03-28745-930

US-10-474-794-277

US-10-474-794-277

US-10-474-794-281

US-60-487-610-2476

US-60-487-610-2330

PCT-US03-28227-4411

US-60-487-610-2330

PCT-US03-28227-4411

US-10-388-457-4

US-10-388-457-4
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CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.0
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98.9%;
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     Similarity
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     NAME/KEY: SIGNAL
      199.5
199.5
198.5
190.5
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Sequence 8, Application US/10398457

Sequence 8, Application US/10398457

GENERAL INFORMATION:
APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.

APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.

TILLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS FILE REPERBNCE: W0465

CURRENT APPLICATION NUMBER: US/10/398,457

CURRENT FILING DATE: 2003-11-13

NUMBER OF SEQ 1D NOS: 37

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REPRESENCE: CLOOK 470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FRAISEQ for Windows Version 4.0
SEQ ID NO 1561
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                                                                                             Length 91;
                                                                                       Query Match
3est Local Similarity 98.9%; Pred. No. 6.4e-46;
4atches 90; Conservative 0; Mismatches 1; Indels
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APPLICANT: CARGILL, Michele
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                         ORGANISM: Homo sapiens
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LOCATION: (1)..(23)
3-10-398-457-8
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                                               -60-487-610-2474
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LENGTH: 91
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TYPE: PRT
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Sequence 10, Application US/10398457
GENERAL INFORMATION: ESSBARCH SYSTEMS ARS HOLDING N.V.
APPLICANT: APPLIED ESSBARCH SYSTEMS ARS HOLDING N.V.
TILLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS FILE REFERENCE: WO465
CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ 1D NOS: 37
SOFTWARE: PATENTIN VEXSION 3.0
                                                                                                                                                                                                                                                                         Sequence 9, Application US/10398457
GENERAL INFORMATION:
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
FILE REFERENCE: WO465
CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.0
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                                       1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                0; Gaps
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0; Gaps
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    2; Indels
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    0; Mismatches
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ORGANISM: Escherichia coli
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Matches 89; Conservative
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ORGANISM: Escherichia coli
      89; Conservative
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US-10-398-457-10
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US-10-398-457-9
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LENGTH: 91
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TYPE: PRT
ORGANISM: Escherichia coli
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Best Local Similarity
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Best Local Similarity
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US-10-398-457-13
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GENERAL INFORMATION:
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
ITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
FILE REFERENCE: WO465
CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ 1D NOS: 37
SOFTWARE: Patentin version 3.0
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GENERAL INFORMATION:
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
FILE REFERENCE: W0465 W0465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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97.5%; Score 466; DB 6; Length 91;
Best Local Similarity 97.8%; Pred. No. 3e-45;
Matches 89; Conservative 0; Mismatches 2; Indels
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61 AVVFVTRKNAQVCANPEKKWVREYINSLEMS 91
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les 89; Conservative
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3-10-398-457-11
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3-10-398-457-12
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S-10-398-457-13
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APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
FILE REFERENCE: W0465.
CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 13
LENGTH: 91
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
FILE REFERENCE: W0465
CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 37
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24 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVPVTRKNRGVCANPEKKWVRE 83
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Best Local Similarity 100.0%; Pred. No. 4.5e-35;
Mismatches 68; Conservative 0; Mismatches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
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APPLICATION NUMBER: US/09/291,038
APPLICATION NUMBER: cunknown>
FILING DATE: L4-Apr-1999
APPLICATION NUMBER: cunknown>
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US/08/615,232A
APPLICATION NUMBER:
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-622-134-11
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APPLICATION NUMBER: US/10/622,134
FILING DATE: 18-7u1-2003
CLASSIFFCATION: 424
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REGISTRATION NUMBER: 550-32
REPERENCE/DOCKET NUMBER: 550-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
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APPLICATION NUMBER: GB 9408602
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRIFFITHS JOHNSON, DAVID A.
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APPLICATION NUMBER: GB 9318984
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ZIP: 22201-4714
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10622134 GENERAL INFORMATION:
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PADLICATION US/10398457

RAL INFORMATION: RESEARCH SYSTEMS ARS HOLDING N.V.

PLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.

PLICANT: APPLIED RESEARCH SYSTEMS MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS

IDE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS

REPRESENCE: WO465

RRENT APPLICATION UNDERF: US/10/398,457

RRENT TILING DATE: 203-11-13

RRENT FILING DATE: 203-11-13

RRENT FILING DATE: 203-11-13

RRENT FILING DATE: 203-11-13
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                                                                                                                                                                                                                                                                                                                                                            Match
Local Similarity 95.0%; Score 454; DB 6; Length 91;
Local Similarity 95.6%; Pred: No. 6.76-44;
tes 87; Conservative 0; Mismatches 4; Indels
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)-398-457-7
                                                                                                                 ARE: Patentin version 3.0 NO 6 ITH: 91
                                                                                                                                                                                                                         MISM: Escherichia coli
fURE:
                                                                                                                                                                                                                                                                                      3/KEY: SIGNAL
ATION: (1)..(23)
98-457-6
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61 YINSLEMS 68
84 YINSLEMS 91
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JUG-312-38A-2

Jequence 2, Application US/10332038A

Sequence 2, Application US/10332038A

SEGUENT Gryphon Therapeutics, Inc.

APPLICANT: Offord, Robin

APPLICANT: Gaerner, Hubert

APPLICANT: Gaerner, Hubert

APPLICANT: Hartley, Oliver

TITLE REFERENCE: 03504-27.

CURRENT APPLICATION NUMBER: US/10/332,038A

CURRENT FILING DATE: 2003-05-06

PRIOR PILICATION NUMBER: US 60/217,683

PRIOR PILING DATE: 2000-07-12

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.2

LENGTH. 68
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Best Local Similarity 100.0%; Pred. No. 4.5e-35;
Matches 68; Conservative 0; Mismatches 0; Indels
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61 YINSLEMS 68

arch completed: December 16, 2003, 15:47:23
b time : 13.4262 secs

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Sequence 12, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 14, Appli
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                                                           December 16, 2003, 15:36:20; Search time 14.4208 Seconds (without alignments) 266.996 Million cell updates/sec
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Sequence 5, Ap
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1 MKVSAARLAVILIATALCAP.....VCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                              lssued_Patents AA:*
1: /cgT2_6/prodata/1/iaa/5A_COMB.pep:*
3: /cgT2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgT2_6/prodata/1/iaa/6A_COMB.pep:*
5: /cgT2_6/prodata/1/iaa/6B_COMB.pep:*
6: /cgT2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgT2_6/prodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stal number of hits satisfying chosen parameters:
                                                                                                                                                                             328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                    ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         1 protein - protein search, using sw model
                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                       inimum DB seq length: 0
                                                                                                       US-09-920-137A-8
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Match Length DB
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>rfect score:
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Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 3, Appli Sequence 13, Appli Sequence 13, Appli Sequence 20, Appli Sequence 20, Appli Sequence 5, Appli Sequence 17, Appli Sequence 17, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli	
28 374 78.2 69 3 US-08-036-922-2 29 374 78.2 69 3 US-08-036-922-3 31 374 78.2 69 4 US-08-036-922-4 32 374 78.2 69 4 US-09-639-081-2 33 374 78.2 69 4 US-09-639-081-3 34 374 78.2 69 4 US-09-639-081-3 35 374 78.2 76 4 US-09-639-081-3 35 374 78.2 76 3 US-08-039-081-3 36 374 78.2 76 4 US-09-639-081-4 36 374 78.2 76 4 US-09-639-081-4 37 370 77.4 67 3 US-09-141-083-2 38 370 77.4 67 3 US-09-141-083-2 39 369 77.2 68 2 US-09-141-083-5 41 366 76.6 68 2 US-08-316-116 41 366 76.6 68 2 US-08-316-180-5 42 363 75.9 66 4 US-09-55-663-2 43 353 75.9 66 1 US-08-336-111-14	RESULT 1 US-08-347-492B-12 is Sequence 12, Application US/08347492B Patent No. 566208 GENERAL INFORMATION: APPLICANT: Wilds, Craig G. APPLICANT: Bandman, Olga APPLICANT: All Porter Drive CURRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CURRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc. STRATE: CA COUNTRY: U.S. ZIP: 940-A10-A10- STRATE: CA CONFUTER: IBM Compatible COMPUTER: Bandsee Version 1.5 COMPUTER: Bandsee Version 1.5 COMPUTER: Bandsee Version 1.5 COMPUTER: Pation All Compatible COMPUTER: 1914 Porter Drive APPLICATION NUMBER: 08/330,011 FILING DATE: 29-NOV-1994 APPLICATION NUMBER: 08/320,011 FILING DATE: 05-COT-1994 APPLICATION NUMBER: 08/320,011 FILING DATE: 05-COT-1994 APPLICATION NUMBER: 08/320,011 FILING DATE: 18-820-0195 INFORMATION FOR SEQ ID NO: 12: SEQUENCE: LIBRARY: GENBARK ILBRARY: GENBARK ILBRARY: GENBARK ILBRARY: GENBARK ILBRARY: GENBARK ILBRARY: GENBARK ILBRARY: GENBARK

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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Coleman, Roger
APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INOYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 478; DB 1; Length 91; 100.0%; Pred. No. 1e-47; tive 0; Mismatches 0; Indels
Query Match
100.0%; Score 478; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                  61 AVVFVTRXNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08375346A Patent No. 5605817 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEC Version 1.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/375,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEPAX: (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,954
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/ABGINT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALO ALTO
CALIFORNIA
RY: USA
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STRANDEDNESS: siz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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STATE:
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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APPLICANT: COLEMAN, ROGER
APPLICANT: STUART, SUSAN G.
TITLE OF INTENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 478; DB 2; Length 91; 100.0%; Pred. No. 1e-47; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Murry, Lynn E.
APPLICANT: Murry, Lynn E.
APPLICANT: MURRY, Lynn E.
APPLICANT: MURRY, Lynn E.
ANGHER OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                      61 AVVFVTRKNRQVCANPEKKMVREYINSLEMS 91
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0063 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,682
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 8, Application US/08421144A; Patent No. 5874211; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REPRENCE/DOCKET NUMBER: PF-06
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-85-055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             Sequence 3, Application US/08633682; Patent No. 5840544; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Best Local Similarity 100.0
Marches 91; Conservative
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-633-682-3
                                                                                                                               US-08-633-682-3
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                                                                                                                                                                                                                                                                                                                                                              STREET:
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Matches
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100.0%; Score 478; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1e-47;

Matches 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144A
FILING DATE: 13-APR-1995
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbard J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: 33954
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEXX: 415-855-0195
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1:08-192-12
Sequence 12. Application US/08798143
Sequence 12. Application US/08798143
Patent No. 593608
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
TITLE OF INVENTION: PRODUCTION AND USES
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYCE Pharmaceuticals, Inc.
STREET: 3174 PORTER Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AVVEVTRKNRQVCANPEKKWVREYINSLEMS 91
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,143
FILING DATE: 10-FEB-1997
CLASSIFFCATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                        3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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MEDIUM TYPE: Diskett
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                STREET: 31/2 .-
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1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Coleman, Roger
APPLICANT: Wilde, Craig C.
APPLICANT: Wilde, Craig C.
APPLICANT: Seilhamer, C. Fortrey J.
TITLE OF INVENTION: A DEFOUNCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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REGISTATION UNBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,123B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,346
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AVVEVTRKNRQVCANPEKKMMEKINSI
APPLICATION NUMBER: 08/347,492
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: 08/33,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-COT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          PF-0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08467123B
Patent No. 5/45506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDICE:
COMPUTER: IBM CC...FO
OPERATING SYSTEM: DOS
OPERATING FASTSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                             LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
| IMMEDIATE SOURCE:
| LIBRARY: GENBANK
| CLONE: GI 134510
US-08-798-143-12
                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
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0; Gaps

0; Indels

0; Mismatches

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91; Conservative
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Matches 91; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIRGINIA
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US-08-836-922-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-395-918-3
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Matches
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                                                                                                                                                                                                                                                                            1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                  100.0%; Score 478; DB 2; Length 91; 100.0%; Pred. No. 1e-47; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.

APPLICANT: Bandman, Olga

APPLICANT: Murry, Lynn E.

CORRESPONDENES: 5

CORRESPONDENESS:
                                                                                                                                                                                                                                                                                                                                                    61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                   61 AVVEVTRKNROVCANPERKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: 33,954
TELEPHONE: 415-855-0555
TELEPHONE: 415-852-0195
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/633,682
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-936-772-3
Sequence 3, Application US/08936772
Patent No. 6015883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
         415-555-0555
                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                               91 amino acids
                                                                                                                                                                                                                                             91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                    single
                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GenBank
CLONE: GI 134510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                 TYPE: amino acid
STRANDEDNESS: Sil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
           TELEPHONE:
                                                                                                                                                                         -08-467-123B-5
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                                                                                   CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                 Matches
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Sequence 14, Application US/08836922
Patent No. 615971
GENERAL INFORMATION:
APPLICANT: INTES PROUDFOOT, AMANDA ELIZABETH
APPLICANT: WELLS, TIMOTHY NIGEL CARL
TITLE OF INVENTION: RANTES PEPTIDE AND FRAMENTS AND
TITLE OF INVENTION: COMPOSITIONS COMPRISING IT FOR TREATMENT OF INFLAMMATION
NUMBER OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDUMYTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                           61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/936,922
FILING DATE: 23 MAY-1997
CLASSIPRICATION: 435
PRIOR APPLICATION NUMBER: GB 9424835.8
FILING DATE: 08-DEC-1994
PRIOR APPLICATION NUMBER: GB 9512319.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE POCKET NUMBER: 1430-163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4011
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 20
CORRESSONDEMESS: AND ADDRESSES: AND ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: GB 9512319.6
FILING DATE: 16-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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SEQ ID NO 3 LENGTH: 91

IYPE: PRT

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91 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy <
                                                                                                                                                                                                                                                                                                                             STATE: VIKG...
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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US-09-639-881-14
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Sequence 25, Application US/09230371A

Patent No. 634856

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Russo, James J

APPLICANT: Moore, Patrick S

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 45185-G-PCT-US

CURRENT APPLICATION NUMBER: US/09/230,371A

CURRENT APPLICATION NUMBER: PCT/US97/13346

PRIOR FILING DATE: 1997-07-22

SOFTWARE: PatentIN Ver. 2.0

SOFTWARE: PatentIN Ver. 2.0
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                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: DNA ENCODING RANTES HOMOLOG FROM PROSTATE
FILE REFERENCE: PF-0653 US
CURRENT APPLICATION NUMBER: US/09/395,918
CURRENT FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 478; DB 4; Length 91; 100.0%; Pred. No. 1e-47; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 478; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AVVFVTRKONROVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: GenBank: GI 134510
3-09-395-918-3
                                                                            Hawkins, Phillip R
  Sequence 3, Application US/09395918 Patent No. 6238666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-09-230-371A-25
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Query Match

Best Loca Matches

SSULT 11

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Sequence 14, Application US/09639881
Patent No. 6555105
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MELLS, TIMOTHY NIGEL CARL
APPLICANT: WELLS, TIMOTHY NIGEL CARL
TITLE OF INVENTION: RAWTES PERTIDE AND FRAGMENTS AND
TITLE OF INVENTION: COMPOSITIONS COMPRISING IT FOR TREATMENT OF INFLAMMATION
CORRESPONDENCE: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKVSAARLAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 478; DB 4; Length 91; Best Local Similarity 100.0%; Pred. No. 1e-47; Matches 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACKOPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPLICATION NUMBER: US/09/639,881
FILING DATE: 17-AUG-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,922
FILING DATE: 23-MAY-1997
PRIOR APPLICATION UNBER: GB 9424835.8
FILING DATE: 08-DEC-1994
PRIOR APPLICATION NUMBER: GB 9721319.6
FILING DATE: 16-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1430-163
                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRICKLY MARE: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 816-4011
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Godiska, Ronald
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Parrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
TITLE OF INVENTION: ANALOGS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.9%; Pred. No. 5.1e-47;
Matches 90; Conservative 0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/660,542
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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                                                                                                                                                                                                                                                                                    ACTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32779
TELEROMUNICATION INFORMATION:
TELEROME: 312/474-6300
TELERA: 35-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Illinois
RY: United States of America
60606-6402
              : Illinois
RY: United States of America
60606-6402
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Sequence 21, Application US/08660542
Patent No. 5932703
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: "RANTES"
3-08-480-449-21
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inear
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CITY: Chicago
                                                                                                                                                                                                                                                 LING DATE
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                                         COUNTRY:
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1 MKVSAAALAVILIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKVSAARLAVILLATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60
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US-08-679-493A-155
US-08-679-493A-155
Sequence 155, Application US/08679493A
Pacent No. 6303295
GENERAL INFORMATION:
APPLICANT: TAYLOX: Ethan W.
TITLE OF INVENTION: SELENDERORIES, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1995-07-12
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 98.7%; Score 472; DB 4; Length 91; 1 Similarity 98.9%; Pred. No. 5.1e-47; 90; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.7%; Score 472; DB 2; Length 91; 98.9%; Pred. No. 5.1e-47; tive 0; Mismatches 1; Indels
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                                                               PATELICATION TOWNER: 08/479,620
FILING DATE: 07-UIN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVIG A.
REGISTRATION NUMBER: 38,153
REFRENCE/DOCKET NUMBER: 27866/33
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-0448
APPLICATION NUMBER: 08/558,658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "RANTES"
                                                                                                                                                                                                                                                                  TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                    FILING DATE: 16-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       feature
                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
LOCATION: 1..68
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc
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61 AUVFUTRKNRQVCANPEKKWVREYINSLEMS 91

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1 MKVSAARLAVILIATALCAPASASPYSSDTTPÇCFAYIARPLPRAHIKEYFYTSGKÇSNP 60
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98.7%; Score 472; DB 4; Length 91;

Best Local Similarity 98.9%; Pred. No. 5.1e-47;

Matches 90; Conservative 0; Mismatches 1; Indels
                                                                                                                        APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: NACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARREST: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 South Macker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDTUM TYPE: FORM:
OMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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)b time : 15.4208 secs
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SULT 15
-08-479-603-21
-08-479-603-21, Application US/08479603
Patent No. 6320023
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPERENCE/DOCKET UNMEER: 27866
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
OTHER INFORMATION: "RANTES"
:-08-479-603-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein - protein search, using sw model

December 16, 2003, 15:36:20; Search time 13.5738 Seconds (without alignments) 651.810 Million cell updates/sec

US-09-920-137A-7 tle: rfect score:

1 MKLCVTVLSLLMLVAAFCSP......VCADPSESWVQEYVYDLELN 92 Gapop 10.0 , Gapext 0.5 **BLOSUM62** oring table: quence:

tal number of hits satisfying chosen parameters: nimum DB seq length: 0 ximum DB seq length: 2000000000

283308 segs, 96168682 residues

arched:

Maximum Match 100% Listing first 45 summaries st-processing: Minimum Match 0% PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

tabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	hage in	-H	macrophage inflamm	macrophage inflamm	Д		ag	monocyte adherence			>	u	ucible	chemoatt	w.	Ω	monocyte chemoattr		ø	monocyte chemoattr	v	_	phocy	eotaxin precursor	ы	ocyti	9 pro	0 prote	monocyte adherence
SUMMAKIES	DI	A31767	573	055	339	567	232	057	C60407	381	553	772	467	320	314	213	191	585	929	C233	5	JC5295	긒	7	C247	4809	4809	3723	955	6040
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	Length	92	92	92	92	93	92	92	50	91	91	4	109	4	$^{\circ}$	66	97	125	66	66	66	66	<u>ω</u>	120	96	96	97	96	116	52
	% Query Match	100.	84.				٠.	_:	_:	Ċ.	Ψ.	Ċ	Ψ.	m.	۲.	۲.	٠.	10	ın.	١.	'n.	35.1	₩.	4	m	m.	φ.	œ.	۲.	25.4
	Score					32		00		45.	42.	97.	92.	85.	83.	80.	78.	74.	72.	72.	72.	170.5	67.				41.		31.	23.
	sult No.	-	7	m	4	'n	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	59

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S42496 S2436 A55984 A53096 TCA3 protein - mou A55984 A53096 A17094 A17004 A17006 A1700	101 2 \$42496 92 2 82436 72 455984 103 2 455984 104 1 ETHUL 95 2 A37034 101 2 1486191 101 2 148148 101 2 148148 101 2 148148 101 2 148148 103 2 A37034 103 2 A37034 103 2 A37034 103 2 ENDSI 103 2 150417 103 2 150417 103 2 150417 103 2 150417 103 2 150417 104 2 A53497 105 2 150417 107 2 150417 108 2 A33497 109 2 A33497 100 2 JH0200	22.7 101 2 S42496 1.5 22.3 72 2 S26984 1.5 22.3 103 2 A553096 2.5 22.3 103 2 A553096 2.5 22.3 103 2 A553096 2.5 22.1 114 1 EFHUL 2.5 20.3 99 2 A37034 2.5 19.9 99 2 A37034 2.5 19.9 10.1 2 146818 80 16.5 114 1 EFHUL 2.5 16.2 103 2 126417 2.5 16.2 103 2 126417 2.5 14.9 100 2 140200 2.5 14.9 100 2 140200 2.5 14.9 100 2 160417 2.5 14.9 100 2 160417 2.5 14.9 100 2 160417 2.5 14.9 100 2 160417 2.5 14.9 100 2 160417 2.5 14.9 100 2 160417 2.5 14.9 100 2 160417 ALIGNMENTS ALIGNMENT
	101 2 92 2 2 72 2 72 2 72 2 72 2 72 2 99 2 2 99 2 2 101 2 101 2 101 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103 2 2 103	110.5 22.7 101 2 110.5 22.6 92 2 108.5 22.3 103 2 107.5 22.1 114 1 107.5 22.1 114 1 107.5 22.1 114 1 107.5 22.1 114 1 10.5 22.1 114 1 10.5 19.9 99 2 10.5 18.6 101 2 10.5 18.6 101 2 10.5 18.7 100 2 10.5 18.7 100 2 10.5 14.9 100 2 10.5 14.5 89 2 10.5 14.5 89 2 10.5 10.5 10.5 10.0 2 10.5 10.5 10.5 10.0 2 10.5 10.5 10.5 10.0 2 10.5 10.5 10.5 10.0 2 10.5 10.5 10.5 10.0 2 10.5

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Cidate: 17-Jul.1992 #sequence revision 17-Jul.1992 #text change 16-Jul-1999 CjAccession: S11685; A32393; S04533; A53885; A30552; PS0303; A27596; I56104 Rigrorum: S11685; A32393; S04533; A53885; A30552; PS0303; A27596; I56104 Rigrorum: Cidate, M.; Lowe, S.; Graham, G.; Pragnell, I.; Plumb, M. Nucleic Acids Res. 18, 5561, 1990 A; Title: Sequence of the murine haemopoletic stem cell inhibitor/macrophage inflammato. A; Reference number: S11685; MUID:91016858; PMID:2216738 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophage inflammatory protein-1-alpha precursor - mouse
N;Alternate names: heparin-binding chemotaxis protein; L2G25B protein; SCI/MIP-1a; SI&
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: C30552
A;Molecule type: mRNA
A;Residues: 1-92 < RRO>
A;Residues: 1-92 < RRO>
A;Crossines: GB:M23503; NID:g533244; PIDN:AAA40148.1; PID:g533245
A;Cross-references: GB:M23503; NID:g533244; PIDN:AAA40148.1; PID:g533245
A;Cross-references: GB:M23503; NID:g533244; PIDN:AAA40148.1; PID:g533245
A;Cross-references: GB:M23503; NID:g533244; PIDN:AAA40148.1; PID:g533245
A;Accession: GB; Z251-Z259, 1988
A;Accession: JL0088; MJD:89067830; PMID:3058856
A;Accession: JL0088
A;Accession: JL0088
A;Accession: JC0088
A;Accession: JC0088
                                                                                           macrophage inflammatory protein 1-beta precursor - mouse macrophage inflammatory protein 1-beta precursor - mouse N.Alternate names: H400; SIS gamma; T-cell activation protein gamma C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: C30552; JiO088; FS0304; S22042
R;Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J. Immunol. 142, 679-687, 1889
A;Title: A family of small inducible proteins secreted by leukocytes are members of sof various activation processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Superfamily: macrophage inflammatory protein
C;Keywords: glycoprotein
F;1-23/Domahin: signal sequence #status predicted <SIG>
F;24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>
F;76/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 24-33,'XX',36,'X',38 <SH2>
R;Paubersies, P.; Lepretre, F.; Bailleul, B.; Grove, M.; Pragnell, I.; Plumb, M.
R;Daubersies, P.; Lepretre, F.; Bailleul, B.; Grove, M.; Pragnell, I.; Plumb, M.
R;Daubersies, P.; Lepretre, F.; Bailleul, B.; Grove, M.; Pragnell, I.; Plumb, M.
A;Description: Sequence of the murine macrophage inflammatory protein 1b gene.
A;Reference number: S22042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:X62502; NID:953126; PIDN:CAA44364.1; PID:953127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Cross-references: GB:M35590; NID:g199696; PIDN: AAA39708.1; PID:g199697
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Pred. No. 5.1e-35;
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76.1%;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-92 <DAU>
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A;Residues: 1-92 <SHE>
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int. Immunol. 6, 149-156, 1994
1; Title: Dynamic changes in mRNA expression of neutrophils during the course of acute in 1; Reference number: 146730; MUID:94198229; PMID:8148323
                                                                                                                             Molecule type: mRNA
Residues: 7-55,'I',57-79,'T',81-92 <MLL>
Cross-references: GB:M57503; NID:9339726; PIDN:AAA36752.1; PID:9339727
Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
Immunol. 142, 679-687, 1989
Title: A family of small inducible proteins secreted by leukocytes are members of a ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clore, G.M.; Lodi, P.J.; Garrett, D.S.; Gronenborn, A.M..

Dmitted to the Brookhaven Protein Data Bank, January 1994

Reference number: AS2206; PDB:HUM

Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue

Comment: This protein is secreted by activated lymphocytes and monocytes. It is bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Superfamily: macrophage inflammatory protein
;Keywords: chemotaxis; cytokine; inflammation
;Keywords: chemotaxis; cytokine; inflammation
;123/pomain: signal sequence Haratus predicted <SIG>
;24-92/Product: macrophage inflammatory protein 1-beta #status experimental
;34-58,35-74/Disulfide bonds: #status experimental
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;Species: Oryctolagus cuniculus (domestic rabbit)
;pate: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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3;Superfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA
;Residues: 1-39,'REASS',46-92 <BRO>
;Cross-references: GB:M23502; NID:9533212; PIDN:AAA36656.1; PID:9533213
                      Title: A novel polypeptide secreted by activated human T lymphocytes. Reference number: A45817; MUID:90038522; PMID:2809212
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Reference number: A30552; MUID:89093958; PMID:2521353
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100.0%; Score 486; DB 1;

Best Local Similarity 100.0%; Pred. No. 2.3e-45;

Matches 92; Conservative 0; Mismatches 0;
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Immunol. 143, 2907-2916, 1989
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Introns: 26/1; 64/2
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1; Residues: 1-92 < MOR>
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                                                                                                                                                                   60 PGVIFLTKRNRQICADSKETWVQEYITDLELN 91
                                                                                                                               61 PAVVEQTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                    LD78-beta protein precursor - human
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A; Residues: 1-93 <NAK>
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A;Status: preliminary
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Residues: 24-33,'XX',36-42 <WOL>
Residues: 24-33,'XX',36-42 <WOL>
Note: 26-Met, 30-Pro, and 39-Thr were also found
Moder: U. Yang, 2.; van Deventer, S.; Manogue, K.R.; Sherry, B.; Cerami, A.
Immunol. 146, 4031-4040, 1991
Time a Genomic structure of murine macrophage inflammatory protein-1-alpha and conservence number: 156104; MUID:91237116; PMID:2033269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: mRNA.
Residues: 24-33, XX', 36-54 <SHE>
Residues: 24-33, XX', 36-54 <SHE>
Wolpe, S.D.; Davatelis, G.; Sherry, B.; Beutler, B.; Hesse, D.G.; Nguyen, H.T.; Moldaw.
Red. 167, 570-581, 1988
Prittle: Macrophages secrete a novel heparin-binding protein with inflammatory and neutr.
Reference number: A27596; MUID:88154745; PMID:3279154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:X53372; NID:954062; PIDN:CAA37452.1; PID:9297531
Note: the authors' translation of the nucleotide sequence differs at several positions Kwon, B.S.; Weissman, S.M.
Kwon, B.S.; Weissman, S.M.
Oc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
Title: CDNA sequence of two inducible T-cell genes.
Reference number: A32393; MUID:89184547; PMID:2784565
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Molecule type: mRNA
Residues: 1-92 <DAV.
Residues: 1-92 <DAV.
Cross -references: EMBL:X12531; NID:g53122; PIDN:CAA31047.1; PID:g53123
Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
Immunol. 142, 679-687, 1989
Title: A family of small inducible proteins secreted by leukocytes are members of a ne
                                                                                                                                                                                                                                                                                                                                                                                 Title: Cloning and characterization of a cDNA for murine macrophage inflammatory prote
Reference number: S04533; MUID:88258380; PMID:3290382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue Note: the sequence has been corrected in reference A53885

Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermsen, K.; Luedke, C.; Gallegos, C.; Exp. Med. 170, 2189, 1989
                                                                                                                                                                                                                                                                                     Cross-references: GB:J04491; NID:9201524; PIDN:AAA40304.1; PID:9201525
Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermsen, K.; Luedke, C.; Gallegos, C.;
Exp. Med. 167, 1939-1944, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :1-23/Domain: signal sequence #status predicted <SIG>
:24-92/Product: macrophage inflammatory protein #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of various activation processes.
Reference number: A30552; MUID:89093958; PMID:2521353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 1-48,'E',50-90,'I',92 <DA2>
Cross-references: EMBL:X12531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This protein is a monokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23/3; 26/1; 63/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reference number: A53885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 56; Conserva
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Residues: 1-92 <RES>
                                                                                                                                                                                                                                           Molecule type: mRNA
Residues: 1-92 < KWO>
Residues: 1-92 <GRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A27596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: PS0303
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                                                                                                                                                                                                                 Accession: A32393
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Matches
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N/Alternate names: macrophage inflammatory protein homolog GOS19-2; small inducible cy
                                                                                                                                                                                                                                                                                                                                    A,Title: Structures of human genes coding for cytokine LD78 and their expression. A,Reference number: A35673; MUID:90287155; PMID:1694014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         macrophage inflammatory protein-lalpha - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                 C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 20-Jun-2000 C;Accession: B35673; B30412; S10157; B30908 R;Nakao, M.; Nomiyama, H.; Shimada, K. Mol. Cell. Biol. 10, 3646-3658, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:D90145; NID:g219907; PIDN:BAA14173.1; PID:g219908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.8%; Score 320; DB 2; Length 93
58.7%; Pred. No. 1.8e-27;
tive 20; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 17q11-17q21
A;Introns: 26/1; 64/2
C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-93/Product: LD78-beta protein #status predicted <MAT>
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Length 92;

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61.8%; Score 300.5; DB 257.6%; Pred. No. 2.3e-25;
F;33-57,34-73/Disulfide bonds: #status predicted
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Best Local Similarity
                                                                                                                                            Best Local Similarity
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Molecule type: mRNA
Fesidues: 1-92 - CaIP-
Molecule type: mRNA
Fesidues: 1-92 - CaIP-
Molecule type: mRNA
Fesidues: 1-92 - CaIP-
Molecule type: mRNA
Fesidues: 1-92 - CaIP-
Fesidues: 1-92 - CaIP-
Molecule type: mRNA
Fesidues: 1-92 - CaIP-
Fesidues: 1-92 - Ca
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Alternate names: LD78-alpha protein precursor; lymphocyte tumor promoter-induced prote
                                                        Shi, M.M.; Godleski, J.J.; Paulauskis, J.D.
ochem. Biophys. Res. Commun. 211, 289-295, 1995
Title: Molecular cloning and posttranscriptional regulation of macrophage inflammatory
Reference number: 152322; MUID:95298037; PMID:7779098
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Biochem. 99, 885-894, 1986.
Title: A CDNA clone used to study mRNA inducible in human tonsillar lymphocytes by a Reference number: A24198; MUID:86223879; PMID:3086300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-references: GB:D90144; NID:g219905; PIDN:BAA14172.1; PID:g219906; Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Slebenlist, U. Immunol. 142, 1582-1590, 1989; Jittle: Mitogenic activation of human T cells induces two closely related genes which ;Reference number: A30574; MUD:89140347; PMID:2521882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Special Mono sapiens (man)
Special Homo sapiens (man)
Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 21-Jul-2000
Accession: A35673; A30574; A30412; A24198; A30908
Accession: A35673; A30574; A30412; A24198; A30908
Nakao, M.; Nomiyama, H.; Shimada, K.
Cell. Biol. 10, 3546-3558, 1990
Trible: Structures of human genes coding for cytokine LD78 and their expression.
Reference number: A35673; MUID:90287155; PMID:1694014
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;1-20/Domain: signal sequence #status predicted <SIG>
;21-92/Product: macrophage inflammatory protein 1-alpha #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNÀ
Residues: 1-92 «RES.
Cross-references: BMBL:U22414; NID:G790632; PIDN:AAA80608.1; PID:G790633
Superfamily: macrophage inflammatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.4%; Score 303.5; DB 2 57.6%; Pred. No. 1.1e-25;
                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PAVVEQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 PGVIFLTKRNRQICADPKETWVQEYITELELN 91
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Matches 53; Conserv
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Molecule type: DNA
Residues: 1-92 <NAK>
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'Residues: 1-92 <OBA>
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                                          Accession: I52322
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A)Cross-references: GB:M21121
C)Comment: The acronym RANTES reflects the description "Regulated upon Activation, No. C)Genetics:
C)Genetics: A)Genetics: A)Genetics: A)Genetics: A)Genetics: A)Genetics: A)Genetics: GB:120749, OMIM:187011
A)Genetics: A)Genetics: GB:120749, OMIM:187011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: C60407
R;Sporn, S.A.; Elerman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haski, J. Imminol. 144, 4434-4441, 1990
A;Tille: Moncyte adherence results in selective induction of novel genes sharing home, A;Reference number: A60407; MUID:90257367; PMID:2341726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C)Accession: A28815
R)Schall, T.J.; Jongerra, J.; Joyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.;
R)Schall, T.J.; Jongerra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.;
Immunol. 141, 1018-1025, 198
A)Title: A human T cell-specific molecule is a member of a new gene family.
A)Reference number: A28815; MUID:88285659; PMID:2456327
A)Molecule type: mRNA
A)Residues: 1-91 <SCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monocyte chemoattractant cytokine RANTES precursor - human
N;Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES
C;Species: Homo sapiens (man)
C;Date: 30-unn-1989 #sequence_revision 16-Aug-1996 #text_change 29-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: macrophage inflammatory protein
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-91/Product: T-cell protein RANTES #status predicted <MAT>
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                                                           1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYBTSSLCSQ 60
                                                                                                   C;Species: Homo sapiens (man)
C;Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 03-May-1996
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1; Gaps
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Local Similarity 45.7%; Pred. No. 1.9e-19;
hes 42; Conservative 23; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-50 <SPO> C;Superfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.1%; Score 263; DB 2; Length 50; 98.0%; Pred. No. 1.4e-21; tive 1; Mismatches 0; Indels
   Indels
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   161
                                                                                                                                                                                                               61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                        19; Mismatches
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61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92

SULT

Tue Dec 16 15:54:08 2003

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Richenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
A;Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the CDNA a A;Reference number: JC1478; MUID:93213290; PMID:8461011
A;Residues: JC1478
A;Molecule type: MRNA
A;Residues: 1-109 < COP2>
A;Cross-references: GB:X72308; GB:S57464; NID:g3928270; PIDN:CAA51055.1; PID:g313708
B;Minty, A.; Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux submitted to the EMBL Data Library, March 1993
A;Rescription: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattr
A;Reference number: S3222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              May the chemotactic protein 3 precursor - human monocyte chemotactic protein 3 precursor - human monocyte chemotactic protein MCP-3

What learnate names: monocyte chemoattractant protein MCP-3

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Accession: A44678; JC1478; S32222

R; Opdenakker, G; Fiten, P.; Nys, G; Froyen, G; Van Roy, N.; Speleman, F.; Laureys, Genomics 21, 403-403, 1994

A; Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the human mCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the first property of 
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A.Cross-references: EMBL.X71087; NID:g288396; PIDN:CAA50405.1; FID:g288397
C.Comment: This protein induces proteinase secretion and chemotaxis by macrophages and
NyAlternate names: monocyte chemoattractant protein-1
C;Species: Rattus norvegicus (Norway rat.)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S07723; JN0128
R;Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res. 18, 23-34, 1990
NyTille: Analysis of the rat JE gene promoter identifies an AP-1 binding site essentia
A;Reference number: S07723; MUID:90174947; PMID:2106664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 26/1; 65/2
C;Superfamily: macrophage inflammatory protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;4-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Yoshimura, T.; Takeya, M.; Takahashi, K.
Biochem. Biophys. Res. Commun. 174, 504-509, 1991
A;Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its
A;Reference number: JN0128; MUID:91128376; PMID:1704226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYE-TSSLCS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: EMBL:X17053; NID:955530; PIDN:CAA34901.1; PID:955531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M57441; NID:g205333; PIDN:AAA63496.1; PID:g205334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 197.5; DB 1; Length 148;
Pred. No. 4.6e-14;
0; Mismatches 33; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 QPAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: spleen cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.6%;
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A; Residues: 1-109 <OPD>
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Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.
1. Cell Baol. 14, 2914-2925, 1994
Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking region
Reference number: 148654; MUID:94217689; PMID:7513046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:U02298; NID:g460090; PIDN:AAA18302.1; PID:g460091
Schall, T.J.; Simpson, N.J.; Mak, J.Y.
T. J. Immunol. 22, 147-1481, 1992
Reference number: A46539; MUID:92289805; PMID:1376260
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Residues: 1-40, E',42-91 <NEI>
Cross-references: GB:M77747; NID:9200649; FIDN:AAA40029.1; FID:9200650
Comment: This chemcattractant for monocytes but not neutrophils is an immediate-early
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Neilson, E.G.; Krensky, A.
dney Int. 41, 220-225, 1992
Title: Isolation and characterization of cDNA from renal tubular epithelium encoding r
Reference number: 156970; MUID:92277990; PMID:1375672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 18-Jun-1993 #sequence revision 16-Aug-1996 #text_change 22-Jun-1999
Accession: 148875; A46539; T48654; I56970
Danoff, T.M.; Lalley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.
Immunol. 152, 1182-1189, 1994
Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene
Reference number: 148875; MUID:94132613; PMID:7507961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-91/Product: monocyte chemoattractant cytokine RANTES #status predicted <MAT>
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Accession: A46.29
Molecule type: mRNA
Residues: 1-18,'A',20-91 <SCH>
Residues: 1-18,'A',20-91 <SCH>
Cross-references: GB:S37648; NID:g250207; PIDN:AAB22330.1; PID:g250208
Experimental source: macrophage cell line PU5-1.8
Experimental source: macrophage cell line PU5-1.8
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Keywords: chemotaxis; cytokine; immediate-early protein; inflammation
1-23/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                     nocyte chemoattractant cytokine RANTES precursor - mouse
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Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                            60 PAVVEVTRKNROVCANPEKKWVREYINSLEMS
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Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Mus musculus (house mouse)
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Matches 45; Conserva
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Residues: 1-91 <SHI>
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Query Match

SULT 11

Gaps

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monocyte chemoattractant protein-1 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: UC2136; S57498
C;Accession: UC2136; S57498
C;Accession: UC2136; S57498
C;Accession: UC2136; Mulb:94, 962-968, 1994
A;Ittle: Dorchen Leural cells express monocyte chemoattractant protein-1 (MCP-1): Anal A;Reference number: UC2136; MulD:94183284; PMID:7510962
A;Accession: UC2136
A;Accession: UC2136
A;Reseidues: 1-99 cHOS>
A;Cross-references: GB:248479; NID:9683716; PIDN:CAA88370.1; PID:9683717
B;Zach, C, the PMB: Date 1:thraw, Int. 1904
J. Immunol. 150, 5025-5032, 1993
A;Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression A;Reference number: 148147, MUID:93267104; PMID:8496603
A;Accession: 148147
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-120 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLCVTVLSLIMLVAAFGSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYE-TSSLCS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKeywords: glycoprotein
P:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted to the EMBL Data Library, July 1994
A,Reference number: S57497
A,Accession: S57498
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 199 - CAAC>
A,Cross references: EMBL:X79416; NID:g872312; PIDN:CAA55945.1; PID:g872313
C,Superfamily: macrophage inflammatory protein
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                                                                                                                                                                                                                      A; Cross-references: GB: L04985; NID: 9349820; PIDN: AAA37047.1; PID: 9349821
                                                                                                                                                                                                                                                                                                                                                                             37.8%; Score 183.5; DB 2; Length 120; 40.7%; Pred. No. 1.2e-12;
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37.1%; Score 180.5; DB 2; Length
Best Local Similarity 35.2%; Pred. No. 2.1e-12;
Matches 32; Conservative 23; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawahara, R.S.; Deuel, T.F.
Biol. Chem. 264, 679-682, 1989
;Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma;Reference number: A44771; MUID:89093129; PMID:2910858
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);Species: Cavia porcellus (guinea pig)

);Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999

);Accession: I48147
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;Molecule type: DNA; mRNA
;Residues: 1-148 <KA2>
;Cross-references: GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:g387169
;Genetics:
                                                     Gene: GDB:SCYA7; SCYA6; MCP-3

Gross-references: GDB:138473; OMIM:158106

Cross-references: GDB:138473; OMIM:158106

Map position: 17q11-17q12

Introns: 36/1, 156/2

Superfamily: macrophage inflammatory protein

Reywords: cytckine; glycoprotein; inflammation

Reywords: cytckine; glycoprotein; inflammation

1-31/Domain: signal sequence #status predicted <AGT>

3-1109/Product: monocyte chemotactic protein 3 #status predicted <MAT>

39/Binding site: carbohydrate (Asn) (covalent) #status predicted
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    Yoshimura, T.

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Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
"A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various J. Immunol. 142:679-687(1989).
             SY04 HUMAN STANDARD; PRT; 92 AA.
P13.25; P22.617; 013-704;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory protein 1-beta) (MIP-1-beta) (T-cell activation protein 2) (ACT-2)
(PAT 744) (H40) (SIS-gamma) (Lymphocyte activation gene-1 protein)
(LAG-1) (H-C21) (G-26 T lymphocyte-secreted protein).
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Lipes M.A., Napolitano M., Jeang K.-T., Chang N.T., Leonard W.J.;
Identification, cloning, and characterization of an immune
activation gene...;
Proc. Natl. Acad. Sci. U.S.A. 85:9704-9708(1988).
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                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=89325421; PubMed=2568930;
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MEDLINE=89093958; Pubmed=2521353;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89140347; PubMed=2521882;
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                                                                                                                                                                                                      (Human)
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                                                                                                                                                                                                        Homo sapiens
SY04 HUMAN
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by multidimensional NMR.";
Science 263:1762-1767(1994).
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.
BINDS TO CORE AND TO CORB. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY COBT. CELES. RECOMBINANT MIP-1-BETA INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNOBERCIENCY VIRUS (SIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- INDUCTION: By mitogens.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lodi P.J., Garrett D.S., Kuscewski J., Tsang M.L.S., Weatherbee J.A., Leonard W.J., Gronenborn A.M., Clore G.M.; "High-resolution solution structure of the beta chemokine hMIP-1 beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of the CC chemokines TARC and macrophage inflammatory protein-1 beta as novel functional ligands for the CCR8 receptor."; Eur. J. Immunol. 28:582-588(1998).
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                                                                                                  The gene encoding the Act-2 cytokine. Genomic structure, HTLV-1/Tax
[6]
SEQUENCE FROM N.A.
MEDLINE=91373378; PubMed=1894635;
Napolitano M., Modi W.S., Cevario S.J., Gnarra J.R., Seuanez H.N.,
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90038522; PubMed=2809212;
Miller M.D., Hata S., Waal Malefyt R., Krangel M.S.;
"A novel polypeptide secreted by activated human T lymphocytes.";
J. Immunol. 143:2907-2916(1989).
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Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR INTERACTION
MEDILNE=98180363, PubMed=9521068,
MEDILNE=98180363, Padrick J., Sozzani S., Luini W., Spinetti G.,
Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
                                                                                                                                                                                                                                            Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P.,
                                                                                                                                  responsiveness of 5' upstream sequences, and chromosomal
                                                                                                                                                                                                                                                                                            Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                Biol. Chem. 266:17531-17536(1991)
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 6-92 FROM N.A. MEDLINE=90038522: Pubmed=?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homodimer
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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STRUCTURE BY NMR.
                                                                                                                                                                   .ocalization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Napolitano M.;
                                                                                               Leonard W.J.;
                                                                                                                                                                                                                                                                                    Lander E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lusso P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNANA AREETZEKA GERTOOOOOOOOOOOOOOOOOOOOOOOOOOOO
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1 MKLCVTVLSILMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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28-FEB-2003 (Rel. 41, Last annotation update)
88-REB-2003 (Rel. 41, Last annotation update)
88-A11 inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                 PROSITE; PSO0472; SMALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T -> C (IN REF. 7).

A -> S (IN REF. 6).

P -> I, (IN REF. 6).

ARKLPR -> I, (IN REF. 2).

ARKLPR -> I, (IN REF. 8).

S -> I (IN REF. 8).

S -> G (IN REF. 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )212 """,
100.0%; Score 486; DB 1; Lengtn >2
""" n*: Pred. No. 6.1e-47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10212 MW; F2EA7CF341B0E258 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PAVVFOTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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EMBL; AC003976; -; NOT_ANNOTATED_CDS.
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                   EMBL; M57503; AAA36752.1; -. PIR; JH0319; A31767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
es 92, Conservative
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                                                                                                                       HGNC:10630; CCL4.
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PDB; 1HUN; 30-APR-94.
PDB; 1JE4; 03-OCT-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00048; ILB;
SMART; SM00199: SCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 AA;
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STRAND
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                                                                                                                         Genew;
MIM; 18
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EMBL, M23502, AAA36656.1; -.
EMBL, M2516, AAA57256.1; -.
EMBL, J04130, AAA51576.1; -.
EMBL, X53683, CAA37723.1; -.
EMBL, X53682; CAA37722.2; ALT_SEQ.

EMBL, X16166; CAA34291.1; -.
EMBL, M69203; AAB00790.1; -.
EMBL, M69201; AAB00790.1; -.
EMBL, M69202, AAB00790.1; JOINED.

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EMBL; U06434; AAA96497.1; -.
HSSP; P13236; 1HUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCL4 OR SCYA4 OR MIP1B.
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74
74
                                                                                C-C) (CHEMOKINE CC)
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les 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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%FTFFF%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory protein 1-beta) (MIP-1-beta)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                  -!- SUBDNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                             SEQUENCE FROM N.A.
STRAIN=New Zealand white;
STRAIN=New Zealand white;
MEDIINE=94198229; PubMed=8148323;
MOTI S., GOLO K., GOLO F., Mutakami K., Ohkawara S., Yoshinaga M.;
Mori S., GOLO K., GOLO F., Mutakami K., Ohkawara S., Yoshinaga M.;
Mori a., Dynamic changes in mRNA expression of neutrophils during the course of acute inflammation in rabbits.";
                                                                                                                                                                                                                                                           Immunol. 6:149-156(1994). PUNCTION: MONOKINE MITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 409; DB 1; Length 92;
Pred. No. 1.9e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine, Chemotaxis; Inflammatory response; Signal.
SIGNAL
SIGNAL
SAMALL INDUCIBLE CYTOKINE A4.
CHAIN
SA 58 BY SIMILARITY.
DISULPID 35 74 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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HSSP; P13236; 1146730.
Interpro; IPR000827; CC_chemkine_sml.
Interpro; IPR001811; Chemokine_ILB.
Pfam; PP00048; ILB; I.
SMART; SM00199; SY; I.
PROSITE; PS00172; SMALL_CYTOKINES_CC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D17402; BAA04226.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 82.6
nes 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHEMOKINE CC)
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                                                                                                                                                                                                                                                                                                                               BY SIMILARITY)
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                                        NCBI_TaxID=9986;
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Best Local S
Matches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-89093958; PubMed=2521353; Brown K.D., Zurawski G.; Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.; A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Macrophage inflammatory SIS-gamma) (ACT2).
-1- SUBUNIT: Homodimer (By similarity).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJNE=89067830; PubMed=3058856; Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G., Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G., Wolpe S.D., Masiarz F., Coit D., Cerami A.; "Resolution of the two components of macrophage inflammatory protein 1, and cloning and characterization of one of those components, macrophage inflammatory protein 1 beta."; J. Exp. Med. 168:2251-2259(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMALL INDUCIBLE CYTOKINE A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A4 precursor (CCL4) (Macrophagé
protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
608451EEEBC7103D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interior IPR000827, CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
Pfam, PF00048; ILB.
SMART; SMO0199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CYTOKINES_CC; 1.
23 SIGNAL
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PAVVFOTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PAVVFLÍKKGRÓICADPSEPWVNEÝVNDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 AA; 10234 MW;
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SEQUENCE FROM N.A. MEDLINE=89184547; PubMed=2784565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91016858; PubMed=2216738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 163:2262-2266(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. 146:4031-4040(1991).
CCL3 OR SCYA3 OR MIP1A.
                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-42.
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                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=DBA/20
                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS.
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   OCCCERRESER PRESERER PRESER PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLCVSALSLLLLVAAFCAPGFSAPMGSDPPTSCCFSYTSRQLHRSFVMDYYETSSLCSK 60
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P10855; P14096;
01-JUL-1989 (Rel. 11, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (Heparin-binding chemotaxis protein) (L2G25B).
                                                                                                                                                                                                                                                                                                                       "Sequence polymorphisms in the chemokines Scyal (TCA-3), Scya2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for each, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: MONOKINE WITH INTLAMMATORY AND CHEMOKINETIC PROPERTIES.
-!- SUBGURIT Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                        STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;
MEDLINE=99370037; PubMed=10438970;
Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
                                           STRAIN=DBA/2J; TISSUE=Liver;
Daubersies P., Lepretre F., Bailleul B., Grove M., Pragnell I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.2%; Score 390; DB 1; Length 92; 76.1%; Pred. No. 2.4e-36; tive 13; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMALL INDUCIBLE CYTOKINE A4.
BY SIMILARITY.
BY SIMILARITY.
BRESFDESIBAC CRC64;
                                                                                                           Plumb M.A.;
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00472; SWALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M35590; AAA39708.1; -. EMBL; X62502; CAA44364.1; -.
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788
7
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SMART; SM00199; SCY; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P13236; 1HUM.
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Blankenhorn E.P.;
                     SEQUENCE FROM N.A.
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Query Match Best Local S Matches 70

۵ <u>ج</u> 1703 MOUSE 10 SY03 MC 10 O10855 11 01-JUL 11 15-SEP 12 Small 13 Dycoteil 15 Chemot

SEQUENCE

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"Sequence polymorphisms in the chemokines Scyal (TCA-3), Scya2 (monocyte chemotrractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for eae7, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=88154745; PubMed=3279154;
Wolpe S.D., Davatelis G., Sherry B., Beutler B., Hesse D.G.,
Wolpe S.D., Davatelis G., Sherry B., Beutler B., Hesse D.G.,
Nguyen H.T., Moldawer L.L., Narhan C.F., Lowry S.F., Cerami A.;
"Macrophages secrete a novel hepatin-binding protein with
inflammatory and neutrophil chemokinetic properties.";
J. Exp. Med. 167:570-581(1988).
-!- FÜNCTION: MONGKINB WITH INPLAMMATORY, PYROGENIC AND CHEMOKINETIC
-!- FÜNCTION: MONGKINB WITH INPLAMMATORY, PYROGENIC AND CHEMOKINETIC
-!- FUNCTION TO A HIGH-AFFINITY RECEPTOR ACTIVATES CALCIUM RELEASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic structure of murine macrophage inflammatory protein-1 alpha and conservation of potential regulatory sequences with a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=BALB/CJ, DBA/2J, NOD/LTJ, SJL/J, and B10.S/J; TISSUE=Spleen;
MEDLINE=99370037; PubMed=10438970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grove M., Lowe S., Graham G., Pragnell I., Plumb M.; "Sequence of the murine haemopoietic stem cell inhibitor/macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
                                                                                                                                                                                                                  MEDLINE-88258380; PubMed=3290382;
Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermsen K., Luedke C., Gallegos C., Coit D., Merryweather J., Ceraml A.;
"Cloning and characterization of a cDNA for murine macrophage inflammatory protein (MIP), a novel monokine with inflammatory and chemokinetic properties.";
J. Exp. Med. 167:1939-1944 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermsen K., Luedke C., Gallegos C., Coit D., Merryweather J., Cerami A.;
J. Exp. Med. 170:2189-2189(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-899093958; PubMed=2521353; Brown K.D., Zurawski G.; Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.; A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes."; J. Immunol. 142:679-687(1989).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGUENCE FROM N.A.
MEDLINE=91237116; PubMed=2033269;
Widmer U., Yang Z., van Deventer S., Manogue K.R., Sherry B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kwon B.S., Weissman S.M.;
"CDNA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory protein 1 alpha gene.";
Nucleic Acids Res. 18:5561-5561(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLCVTVLSILMLVAAFCSPALSAPMGSDPFTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, AND PANCREAS.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
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P16619, Q96168;

P10 AGG-1990 (Rel. 15, Created)

P1-AGG-1990 (Rel. 15, Last sequence update)

P1-AGG-1990 (Rel. 15, Last sequence update)

Small inducible cytokine A3 like 1 precursor (Tonsillar lymphocyte protein) (G0/G1 switch regulatory protein 19-2) (G0S19-2 protein) (RAT 464.2).

CCL3L1 OR SCYALLI OR GOS19-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 320.5; DB 1; Length 92; Pred. No. 1.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMALL INDUCIBLE CYTOKINE A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 AA; 10345 MW; 8BFF2DE7C6DEDD38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
F -> L (IN REF. 3).
V -> A (IN REF. 3).
                                                                                                                                                                                                                                                                 EMBL, AF065939; AAC17506.; .

EMBL, AF065940; AAC17507.1; .

EMBL, AF065941; AAC17508.1; .

EMBL, AF065942; AAC17508.1; .

EMBL, AF065943; AAC17500.1; .

EMBL, AF065943; AAC17510.1; .

EMBL, AF065943; AAC17510.1; .

EMBL, AF065949; F.CHEMOKINE ACLIVITY; IDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PGVIFLTKRNRQICADSKETWVQEYITDLELN 91
                                                                                                                                                                                                                                                                                                                                                                                           Interpro, IPR000827; CC chemkine sml. Interpro; IPR010811; CA chemkine sml. Pfam; PF00048; ILB; 1.
                                                                                                                                                                                                  65.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similaricy
es 56; Conservative
                                                          C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C.C) (CHEMOKINE CC). STRONG, TO SCYA3.
                                                                                                                                                                                                                                                                                               MEDLINE-91103879; PubMed-2271120;
Blum S., Forsdyke R.E., Forsdyke D.R.; "Three human homologs of a murine gene encoding an inhibitor of stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Irving S.G., Zipfel P.F., Balke J., McBride O.W., Morton C.C., Burd P.R., Siebenlist U., Kelly K.;

"Two inflammatory mediator cytokine genes are closely linked and variably amplified on chromosome 17q.";

Nucleic Acids Res. 18:3261-3270(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=90287155; PubMed=1694014;
Nakao M., Nomiyama H., Shimada K.;
"Structures of human genes coding for cytokine LD78 and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pancreas, and Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 10:3646-3658(1990).
MEDLINE=90287702; PubMed=1972563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol. 9:589-602(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC007783; AAH07783.1; -. EMBL; BC027888; AAH27888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X52149; CAA36397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D90145; BAA14173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M24110; AAA35859.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P13236; 1HUM.
Genew; HGNC:10628; CCL311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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RESULT 8
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                                                                                                                                                                                                                                                                1 MKLCVIVLSLLMLVAAFÇSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                    MEDLINE=96181056; PubMed=8607872; Shibata F., Kato H.; Makagawa H., Shiota S., Takano K., Shibata F., Kato H.; Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.; Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.; Shiota S., Takano K., Shibata F., Kato H.; Shiota S., Takano K., Shibata S., Shibat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
8-Rall inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shi M.M., Godleski J.J., Paulauskis J.D.; "Molecular cloning and posttranscriptional regulation of macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Long Evans; TISSUE-Lung;
MEDLINE=9538980; PubMed=772328;
Shanley T.P., Schmal H., Friedl H.P., Jones M.L., Ward P.A.;
Shanley T.P., Schmal H., Friedl H.P., Jones M.L., Ward P.A.;
"Role of macrophage inflammatory protein-1 alpha (MIP-1 alpha) in
                                                                            SMALL INDUCIBLE CYTOKINE A3 LIKE 1.
                                                                                                                                                                                         DB 1; Length 93;
1.3e-28;
                                                                                                                                   L -> P (IN REF. 4; AAH07783).
A7A79E774006D61E CRC64;
                                                                                                                                                                                                                             18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory protein-1 alpha in alveolar macrophages.";
Biochem. Biophys. Res. Commun. 211:289-295(1995)
                                                                                                                                                                                                                                                                                                                                                                    61 PAVVFQTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 AA.
                                                                                                                                                                                                                                 20; Mismatches
                                                                                              BY SIMILARITY BY SIMILARITY
                                                                                                                                                                                             Score 320;
        SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
                                                                                                                                                                                                                 .
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Lung;
MEDLINE-95298037; Pubmed=7779098;
                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acute lung injury in rats.";
J. Immunol. 154:4793-4802(1995).
                                            Cytokine; Chemotaxis; Sīgnal.
                                                                                                                                                         93 AA; 10161 MW;
                                                                                                                                                                                             65.8%;
                                                                                                                                                                                                               58.7%;
                                                                                                                                                                                                                                   54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein 1-alpha) (MIP-1
CCL3 OR SCYA3 OR MIP1A.
                                                                                93
74
91
                                                                23
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                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                  3.5
3.5
3.5
3.5
3.5
                                                                                                    DISULFID
                                                                                                                                         CONFLICT
                                                                                                                         DISULFID
                                                                                                                                                                                                 Query Match
                                                                    SIGNAL
                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-SED-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
protein 1-alpha (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha
protein) (GG/GI switch regulatory protein 19-1) (GOS19-1 protein)
(SIS-beta) (PAT 464.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89140347; PubMed=2521882;
Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;
Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;
"Mitogenic activation of human T cells induces two closely related
genes which share structural similarities with a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obaru K., Fukuda M., Maeda S., Shimada K.;
"A cDNA clone used to study mRNA inducible in human tonsillar lymphocytes by a tumor promoter.";
"J. Blochem. 99:885-894(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 303.5; DB 1; Length 92; Pred. No. 8.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMALL INDUCIBLE CYTOKINE A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

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BY SIMILARITY.

- Y (IN REF. 2 AND 3).

14E861C647F9AZEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PGVIFLTKRNRQICADPKETWVQEYITELELN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 AA
                                                                                                                                                                                                                                                                            EMBL, U06435; recovery 152322.
PIR, 153322; 152322.
HSSP, P13236; 1HUM.
InterPro, 1PR000827; CC chemkine sml.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCL3 OR SCYA3 OR GOS19-1 OR MIPIA.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86223879; PubMed=3086300;
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J. Immunol. 142:1582-1590(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
10335 MW;
                                                                                                                                                                                                                                                      EMBL; U22414; AAA80608.1; -.
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C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
73
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TaxID=9606;
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P10147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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GO:0003800; F:antiviral response protein activity; TAS.
GO:000809; F:chemokine activity; TAS.
GO:0004971; F:signal transducer activity; TAS.
GO:0006961; F:signal transducer activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S., Czaplewski L.G., Dexter T.M., Drummond A.H., Gearing A.H., Heyworth C.M., Lord B.I., McCourt M., Varley P.G., Wood L.M., Edwards R.M., Lewis P.J., Belloolo: an active variant of human macrophage inflammatory protein-1 alpha with improved pharmaceutical properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EINCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.
BINDS TO CCR1, CCR4 AND CCR5, ONE OF THE MAJOR HIV-SUPPRESSIVE
BACTORS PRODUCED BY CD8-4 T CELLS. RECOMBINANT MIP-1-ALPHA INDUCES
A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2,
AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
BUGGELLOLAR LOCATION: Secreted.
INDUCTION: BY TPA OR PHA (TPA = 12-O-TETRADECANOYL PHORBOL-13
ACETAIE (TUMOR PROMOTER); PHA = PHYTOHEMAGGIUTININ (T-CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                MEDLINE=91103879; PubMed=2271120;
Blum S., Forsdyke R.E., Forsdyke D.R.;
"Three human homologs of a murine gene encoding an inhibitor of stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells."; Science 270:1811-1815(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96106406; PubMed=8525373;
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                              Nakao M., Nomiyama H., Shimada K.;
"Structures of human genes coding for cytokine LD78 and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jang J.S., Kim B.E.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49. MEDLINE=96127782; PubMed=8541527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-C) (CHEMOKINE CC). STRONG, TO SCYA3L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-40 AND 71-83, AND FUNCTION.
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EMBL, M23452, AAA50316.1; --
EMBL, M25154, AAA57255.1; --
EMBL, X04754, CAA27388.1; --
EMBL, X04018; CAA27643.1; ALT_SEQ.
EMBL, M22174, AAA3588.1; --
EMBL, D90144; BAA14172.1; --
EMBL, AP043339, AAC03539.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 10:3646-3658(1990).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=90287155; PubMed=1694014;
                                                                                                                                                  cell proliferation.";
DNA Cell Biol. 9:589-602(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 23-92 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:10627; CCL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1B50; 22-JUL-99.
PDB; 1B53; 22-JUL-99.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       expression.
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0007186; P:exceptosis; TAS.
GO; GO:0007186; P:exceptosis; TAS.
GO; GO:0006955; P:inflammatory response; TAS.
GO; GO:0007011; P:regulation of cytoskeleton; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0008166; P:viral replication; TAS.
GO; GO:0008166; P:viral replication; TAS.
InterPro; IPR00827; CC chemistic sml.
InterPro; IPR001811; Chemokine_ILB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090826; 0910C9; 0910C9; 01.00 Created) 01.00V-1997 (Rel. 35, Created) 01.00V-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Small inducible cytokine A4 homolog precursor (Macrophage inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-55369710; PubMed=7642115;
Petrenko O., Ischenko I., Enrietto P.J.;
Fetranko O., Ischenko I., Enrietto P.J.;
Forbation of a cDNA encoding a novel chicken chemokine homologous to miscalbation macrophage inflammatory protein-1 beta.";
Gene 160:305-306(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ČCL4 OR SCYA4.
Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Hughes S.M., Bumstead N.;
Mapping of the gene encoding the chicken homologue of the mammalian chemokine SCYA4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petrenko O., Enrietto P.J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                 pfam; PF00048; IL8; 1.
SMAZT; SMO199; SCY; L.
PROSITE; PS00472; SWALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 92;
                                                                                                                                                                                                                                                                                                                                                                            61.8%; Score svor.,
57.6%; Pred. No. 1.8e-26;
rive 19; Mismatches 19; Indels
                                                                                                                                                                                                                                                                      SMALL INDUCIBLE CYTOKINE A3.
                                                                                                                                                                                                                                                                                                                  D->A: IN BB-10010; IMPROVED PHARMACEUTICAL PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                   517865D5D6776CA8 CRC64;
GO:0006874; P:calcium ion homeostasis; TAS.
GO:0006928; P:cell motility; TAS.
GO:0007267; P:cell-cell signaling; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 PGVIFLTKRSRQVCADPSEEWVQKYVSDLELS 91
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                   92 AA; 10085 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                               53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein 1-beta homolog).
                                                                                                                                                                                                                                                                            92
73
49
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                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
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DISULFID
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VIVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
8-Mail inducible cytokine A5 precursor (CCLS) (T-cell specific RANTES
protein) (SIS-delta).
                                    -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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"Cloning of Bos taurus RANTES mRNA.";
"Cloning of MaR-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
SMALL INDUCIBLE CYTOKINE A4 HOMOLOG.
BY SIMILARITY.
BY SIMILARITY.
AY SIMILARITY.
A > L (IN REF. 1).
SOAF9679A267408F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%; Score 264; DB 1; Length 90;
51.1%; Pred. No. 1.8e-22;
Live 20; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 FOTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 FITRKGREVCANPENDWVQDYMNKMELN 90
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
InterPro; IPR001811; Chemokine_ILB.
SMART; SM00199; SCY, 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
       SUBUNIT: Homodimer (By similarity).
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                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ243034; CAB45103.1; -.
HSSP; P13236; 1HUM.
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                                                                                   C-C) (CHEMOKINE CC).
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72
87
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Best Local Similarity
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Matches
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99228475; PubMed=10213461; Noura R., Yoshie O.; Nonyama H., Pukuda S., Iio M., Tanase S., Mura R., Yoshie O.; Nomyama H., Pukuda S., Iio M., Tanase S., Imman chromosome "Organization of the chemokine gene cluster on human chromosome Inglia. Containing the genes for CC chemokine MPIF-1, HCC-2, LEC, and Inglia. 2 containing the genes for CC chemokine MPIF-1, HCC-2, LEC, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ
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"A human T cell-specific molecule is a member of a new gene family.";
J. Immunol. 141:1018-1025(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYOS HUMAN STANDARD, PRT, 91 AA.
P1301, 043646; 091772,
101-1040-1990 (Rel. 1917, Last sequence update)
115-JUL-1999 (Rel. 38, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (Sig-delta) (T cell-specific protein P228) (TCP228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Zeng Q.P., Yang R.Y., Fu L.C.;
Leng Q.P., Yang R.Y., Fu L.C.;
Submitted Capabance of human beta-chemokine RANTES mRNA.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.7%; Score 246.5; DB 1; Length 91; 48.9%; Pred. No. 1.6e-20; Live 20; Mismatches 26; Indels 1
                                                                                                                                                                                                                                                                                                           InterPro; IPKUULOL.,
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
PROSITE; PS00472; F-cell; Signal; Inflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMALL INDUCIBLE CYTOKINE AS. BY SIMILARITY.
BY SIMILARITY.
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660DD38E015B0735 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interferon Cytokine Res. 19:227-234(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                       HSSP; P13501; 1RTN.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
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MEDLINE=88285659; Pubmed=2456327;
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33 57 B<sup>3</sup>
34 73 B<sup>3</sup>
91 AA; 10073 MW;
                                                                                                                                                                                          EMBL; AJ007043; CAA07430.1; -.
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                                                                                                                                                                                                                                                                                                                                                                    Genew;
MIM; 18
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                   MEDLINE-E1598229.

MEDLINE-E1598229.

RIAUSDERG R.L., Feingeld 12.7. Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdan T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdan T.B., Toshlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Grene E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse CDNA sequences "...

Rodriguez C.DNA sequences" A 94-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PECTATION: CHEMOATRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CILLS AND EGSINOPHILS. CAUGES THE RELEASE OF HISTAMINE FROM BASOPHILS AND EGSINOPHILS. CAUGES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EGSINOPHILS. BINDS TO CCR1, CCR3, CCR4 A CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CB4. CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CB4. INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
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Hoover D.M., Shaw J., Gryczynski Z., Proudfoot A.E.I., Wells T.N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lubkowski J.; "The crystal structure of Met-RANTES: comparison with native RANTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=99111238, PubMed=9889151,
Wilken J., Hoover D., Thompson D.A., Barlow P.N., McSparron H.,
Picard L., Wlodawer A., Lubkowski J., Kent S.B.,
Trotal chemical synthesis and high-resolution crystal structure of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chung C.-W., Cooke R.M., Proudfoot A.B.I., Wells T.N.C "The three-dimensional solution structure of RANTES."; Biochemistry 34:9307-9314(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHESIS, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 49-56; 71-79 AND 83-91, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR.
MEDLINE=95352612; PubMed=7542919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95244456; PubMed=7537088;
       MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96106406; PubMed=8525373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR.
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C-C) (CHEMOKINE CC).

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0003800; F:antiviral response protein activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMALL INDUCIBLE CYTOKINE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GG; GG: 0006874; F: chemotine activity; TAS.
GG; GG: 0006874; F: chemotine activity; TAS.
GG; GG: 0006875; F: cell adhesion; TAS.
GG; GG: 0007267; F: cell activity; TAS.
GG; GG: 0006928; F: cell activity; TAS.
GG; GG: 0006928; F: cellular defense response; TAS.
R GG; GG: 0006935; F: cellular defense response; TAS.
R GG; GG: 0006935; F: cercytosis; TAS.
R GG; GG: 0007655; F: cercytosis; TAS.
R InterPro; IPR000827; CC chemkine Gml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A -> R (IN REF. 1 AND 4).
A -> V (IN REF. 4).
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                                                                                                                                                                                    EMBL, AF043341, AAC03541.1; -.
EMBL, AF088219, AAC63331.1; -.
EMBL, AF266753, AAF73070.1; -.
EMBL, BC008600, AAH08600.1; -.
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                                                                                                                                                          EMBL; M21121; AAA36725.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:10632; CCL5.
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SMART; SM00199; SCY; 1
                                                                                                                                                                                                                                                                                                                                                                                                PDB; 1RTO; 03-JUN-95.
PDB; 1B3A; 23-APR-99.
PDB; 1EQT; 19-APR-00.
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PDB; 1HRJ; 14-OCT-96
PDB; 1RTN; 03-JUN-95.
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79
91 AA;
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P30882;
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SY05_MOUSE
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Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
Krensky A.M., Neilson E.G.;
"Isolation and characterization of cDNA from renal tubular epithelium
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                          15-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A5 precursor (CCLS) (T-cell specific RANTES
protein) (SIS-delta) (MuRantes)
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MEDLINE=94132613; PubMed=7507961;
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Cloning, genomic organization, and chromosomal localization of the
ScyaS gene encoding the murine chemokine RANTES.";
J. Immunol. 152:1182-1189(1994).
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Mol. Cell. Biol. 14:2914-2925(1994).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,
Paznekas W.A.;
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update
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PubMed=12466851;
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Kidney Int. 41:220-225(1992).
                                                                                                                                                                                                                    (Mouse)
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Ronagaya A., Karochkin I.V. Lee Y., Jenhard B., Dyons P.A.,
Ragaboit D.R., Malatale L., Mench Common, Magnatical G.,
Ragaboit C.D.R., Malatale L., Mench Common, Magnatical G.,
Ragaboit C.R., Stringer R., Pontine J. G. (10 to L.) Read of M. S.,
Ragaboit C.R., Schold C., Read J., Rold G. Ring B.Z., Ringwald M.,
R. Sandelin M., Schneider C., Semple C.A., Seroul B. Zhinada K.,
Radalana R., Takenska Y., Taylor M.S., Tasadale R.D., Tonita M.,
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Radalana R., Takenska Y., Taylor M.S., Tasadale R.D., Tonita M.,
Radalana R., Takenska Y., Taylor M.S., Tasadale R.D., Tonita M.,
Radalana R., Takenska Y., Taylor M.S., Tasadale R.D., Radalana M.,
Radalana R., Takenska Y., Taylor M.S., Tasadale R.D., Radalana R.,
Radalana R., Takenska K., Saska R.D., Sanka R., Ankana R.,
Radalana R., Takenska K., Saska R.D., Sanka R., Lander E.S., Rogere J.,
Radalana R., Takenska K., Saska R.D., Sanka R.C., Sanka R.D.,
Radalana Y., Malana R.D., Radalana R., Radalana K., Radalana R.D.,
Radalana R., Takenska R., Saska R.D., Sanka R.D., Sanka R.D.,
Radalana Y., Calabar B. B., Bonaldo M.F., Calabar R.D.,
Radalana Y., Galaria R.D., Gorse L.H., Derge J.G., Indy B.R.,
Radalana Y., Radalana R.D., Sankara R., Lux, Sankar R.C., Sancha R.D.,
Radalana R., Sankar R.D., Sanka R.D., Sanka R.D.,
Radalana R., Marana M., Rodergram E.J., Lux, Glabs R.A.,
Radalana R., Marana M., Radalana M., Radalana R., Radalana R.,
Radalana R., Marana M., Radalana M., Radalana R., Radalana R.,
Radalana R., Marana R., Radalana R., Radalana R., Radalana R.,
Radalana R., Marana R., Walana R., Radalana R., Radalana R.,
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SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOXINE CC).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blanco J.C., Pletneva L.M., Prince G.A.;
"Sigmodon hispidus cytokines, chemokines and interferons.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUGES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
             PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; T-cell; Signal; Inflammatory response.
SIGNAL 1 21 POTENTIAL.
CHAIN 24 91 SMALL INDUCIBLE CYTOKINE AS.
                                                                                                                                                                                                                                       49.9%; Score 242.5; DB 1; Length 91;
                                                                                                                                                                                                                                                 4.4e-20;
hes 26; Indels
                                                                                                                                                                                                                                                                                                                                                                  61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                               60 LAVVEVTRRNROVCANPEKKWVĢEYINYLĒMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AA.
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           igmodon hispidus (Hispid cotton rat).
                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF421391; AAL16932.1; -.
InterPro; IPR000927; CC chemkine sml.
InterPro; IPR001811; Chēmokine_IE8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
           Interpro, IPR000827; CC_chemkine_sml.
Interpro, IPR001811; Chemokine_ILB.
                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                        48.98;
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
MGD; MGI:98262; Ccl5.
                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TaxID=42415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein).
CCLS OR SCYAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGHI
                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
DISULFID
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                              1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                              1 MKISAAVLTVVLMAASLCAPASASPNGSD-TIPCCFAYLSAVLPRAHVKEYFYTSSKCSN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5103-LAYEO 059076;
9107-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
81-RED-2003 (Rel. 41, Last annotation update)
83-FEB-2003 (Rel. 41, Last annotation update)
8mall inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A., Yamaguchi K., Kanazawa M.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
NCBI_TaxID=10141,
                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.1%; Score 238.5; DB 1; Length 91; 49.5%; Pred. No. 1.2e-19; tive 20; Mismatches 25; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 234.5; DB 1; Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Dunkin-Hartley;
Campbell E.M., Proudfoot A.E.I., Yoshimura T., Allet B.,
Wells T.N.C., White A.M., Westwick J., Watson M.L.;
Submitted (NOV-1996) to the EMB/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIÁL.
SMALL INDUCIBLE CYTOKINE
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7F6A31B751237DB9 CRC64;
34 73 BY SIMILARITY.
91 AA; 10082 MW; DODGEAEABE4242FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AA.
                                                                                                                                                                                                                                                                                                                                                     60 FAVVFVTRRNRQVCANPKKKWVQEYINYLEL 90
                                                                                                                                                                                                                                                                                                                61 PAVVFQTKRSKQVCADPSESWVQEYVYDLEL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AB002662; BAA19604.1; -.
HSSP; P13501, 1RTN.
InterPro; IPR001827; CC chemkine sml.
InterPro; IPR001811; Chemokine_ILB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U77037; AAC53293.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.3%;
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SIS-delta).
                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCLS OR SCYAS
                                                                                                                                             45;
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   DISULFID
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                                                                                    Query Match
                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLCVTV-LSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                    STRAIN-LONG Evens; TISSUE-Lung;
Jones M.L., Shanley T.P., Ward P.A.,
Jones M.L., Shanley T.P., Ward P.A.,
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CHEWOATTRACTRACTR FOR BLOOD MONOCYTES, MEMORY T HELPER
-!- FUNCTION: CHEWOATTRACTRACTRON ELOOD MONOCYTES, MEMORY T HELPER
-!- STOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SWALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
8-FBB-2003 (Rel. 41, Last annotation update)
8-FBB-2003 (Rel. 41, Last annotation update)
8-FBB-2003 (Rel. 41, Last annotation update)
9-FBB-2003 (Rel. 41, Last annotation update)
9-FBB-2003 (Rel. 41, Last sequence update)
9-FBB-2003 (Rel. 41, Last sequence update)
                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THEOFRO, TREADERS, CC_cheakine_sml.
InterPro; IPR001811; Chemokine_1E8.
SMART; PF00148; 118. 1.
PROSITE; PF00448; 128. 1.
PROSITE; PF00472; SMALL CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; T-cell; Signal; Inflammatory response.
SIGNAL
CHAIN
25 92 SMALL INDUCELE CYTOKINE A5.
DISULFID 34 BY SIMILARITY.
DISULFID 35 PR SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.1%; Score 229; DB 1; Length 92; 47.3%; Pred. No. 1.4e-18; tive 21; Mismatches 26; Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 58 BY SIMILARITY.
35 74 BY SIMILARITY.
92 AA; 10170 MW; B4FBEC2B4208ABC6 CRC64;
             Pred. No. 3.3e-19;
                                                                                                                                                                                                                                      61 PAVVFOTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                     60 LAVVFVTRKNROVCANPEKKWVREYINSLEMS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 AA.
45.7%; Pred worrarive 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 47.3
nes 44; Conservative
                                                42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-C) (CHEMOKINE CC)
          Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein) (SIS
CCLS OR SCYAS
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P50231;
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60 NLAVVEVTRRNRQVCANPEKKWVQEYINYLEMS 92

60 OPAVVFOTKRSKOVCADPSESWVOEYVYDLELN 92

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Search completed: December 16, 2003, 15:38:21 Job time : 10.5574 secs
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December 16, 2003, 15:36:20 ; Search time 30.6667 Seconds (without alignments) 774.158 Million cell updates/sec
                                                                                                                                                                                                    1 MKLCVTVLSLLMLVAAFCSP......VCADPSESWVQEYVYDLELN 92
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein - protein search, using sw model
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
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sp_bacteriap:*
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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                                                                                                                                                                       US-09-920-137A-7
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                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                            oring table:
                                                                                                                                                                                           rfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tabase :
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                                                                                                           n on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q8nhw4 homo sapien	Q8hyq2 macaca mula	Q91z10 sigmodon hi	Q8sqa6 bos taurus	Q91z65 sigmodon hi	Q8hyq3 macaca mula	Q14745 homo sapien	Q9pwa6 gallus gall	Q8hyn3 macaca mula	Q8hyn4 macaca mula	Q9i8e0 gallus gall	Q8mkd0 equus cabal	Q8hyq1 macaca mula	Q8qg57 gallus gall	canis	Q8sq40 felis silve	
SUMMARIES		ID	O8NHW4	Q8HYQ2	091210	Q8SQA6	091265	Фвну03	014745	Q9PWA6	Q8HYN3	Q8HYN4	Q918E0	Q8MKD0	Q8HYQ1	Q8QG57	QBHYSO	Q8SQ40	
		DB	4	G	11	ø	11	9	4	13	ø	ø	13	9	9	13	9	9	
		Length	92	92	92	66	92	92	80	06	4.9	26	89	91	91	91	91	92	
	æ	Query Match	96.3	94.4	77.4	65.8	9.09	57.9	55.9	54.3	51.9	51.2	50.5	50.1	49.5	48.0	46.4	46.1	
		Score	468	459	376	320	294.5	281.5	271.5	264	252	249	245.5	243.5	240.5	233.5	225.5	224	
		esult No.		10	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	

Q8hyp8 macaca mula Q8qg56 gallus gall	Ogcams muscuiu		Q9ttq4 equus cabal		8 equus o	macaca	_	bos tau	macaca		Q9ttq2 equus cabal	bos taurus	Q98158 kaposi's sa	ratt	Q9ttq1 equus cabal	Q8jim5 paralichthy	Q8av56 paralichthy	parali			rattus	guine	Q8hyp4 macaca mula	ч	Q8ayb2 ictalurus p	092318 cavia porce	5
13	148 11 090YD7	9 66	9	9	9	v	φ	9	9	9	81 6 Q9TTQ2	9	12	11	9	13	13	13	y y	11	11	101 12 Q8JRS7	9	11	95 13 OBAYB2	-	1
204 42.0 189.5 39.0		179.5 36.9	m	m	m	.5	m	34	~	164 3	m	160 32	(*)	(*)		171	رب س	in	5		7.5	10	136) .	133.5 27.5
17	19	202	22.	23	24	25	26	27	28	29	0					100	36	3.7	89 M	68	40	41	4 2	. 4	4 4	: :	4° O

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Nibbs R.J., Barcellos L.F., Townson J.R.;

"Variation in gene copy number of the human chemokines macrophage inflammatory protein-la/CCL3 and macrophage inflammatory protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.3%; Score 468; DB 4; Length 92; 96.7%; Pred. No. 1.8e-49; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                      1b/CCL4.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, 34709147; AAL87008.1;
InterPro; IPR001817; CC chemkine sml.
InterPro; IPR001811; Chemckine_IL8.
Pfam; PR00148; IL8; 1.
PROSITE; PR00149; SCY; 1.
PROSITE; PR00472; SYALL CYTOKINES CC; 1.
SEQUENCE 92 AA; 10166 MW; 4C8D01E926CDE882 CRC64;
                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PAVVEOTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PAVVFQTKRGKQVCADPSESWVQEYVYDLELN 92
                                                                                                                  Macrophage inflammatory protein-1b2.
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89; Conservative
                                PRELIMINARY;
                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                  Q8NHW4;
                                Q8NHW4
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RESULT 1
                O8NHW4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sigmodon hispidus (Hispid cotton rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                         Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                 Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A., "Comprehensive cloning and sequencing reveals evolutionary conservation among all groups of rhesus macaque chemokines."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF449267; AAN76071.1: - SEQUENCE 92 AA: 10103 MW; 80B2C2071565F809 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 17.4%; Score 376; DB 11; Length 92; Local Similarity 71.7%; Pred. No. 3.1e-38; Anders 66; Conservative 13; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blanco J.C., Pletneva L.M., Prince G.A.; "Sigmodon hispidus cytokines, chemokines and interferons."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.4%; Score 459; DB 6; Length 92; 93.5%; Pred. No. 2.3e-48; ative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF421392; AAL16933.1; -...
HSSP; Q9Y58; 1G2S.
InterPro; IPRO01801; CC_chemkine_sml.
InterPro; IPRO0181; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
SEQUENCE 92 AA; 10195 MW; A34FDE21B6FA9C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein 1 beta.
MIP-1BETA.
                                       01-NAR-2003 (TrEMBLrel. 23, Created)
01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PAVVFOTKRGKOVCADPSETWVOEYWNDLELN 92
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es 86; Conservative
                                                                                                                                 Chemokine CCL4/MIP-1BETA.
                                                                                                                                                                                                                                       Cercopithecinae; Macaca.
NCBI_TaxID=9544;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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   Q8HYQ2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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"Sigmodon hispidus cytokines, chemokines and interferons.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AV659407; AAL26704.1; -.
HASSP, G9YZ58; 1G2.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
                                                                                                                                                                                                                                                                                                                                                                                                                      65.8%; Score 320; DB 6; Length 93; 60.9%; Pred. No. 2.2e-31; Live 14; Mismatches 22; Indels
                                                                                                                                                                                                                                                    "Role of chemokines in RSV infection.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY077840; AAL786060.1;
Interpro; IPR001827; CC_chemkine_sml.
Interpro; IPR001811; Chemokine_ID8.
PF00048; ID8; 1.
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                                                                                                                                                                                                                                                                                                                                                            SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 93 AA; 10118 MW; 1266BFBFCEESEBE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
MACCOPAGE inflammatory protein-1 alpha.
MIP1 ALPHA.
                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last Sequence update)
01-OCT -2002 (TrEMBLrel. 22, Last annotation update)
Macrophage inflammatory protein-1 alpha.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                          93 AA
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SEQUENCE 92 AA; 10334 MW; CF9AAB3D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sigmodon hispidus (Hispid cotton rat).
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                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.9% Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
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RESULT 4
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Local Similarity
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Best Local Similarity
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                                                   CHAIN
NON TER
SEQUENCE
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Signal.
NON TER
SIGNAL
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Q8HYN3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MQVSTAALAVLLCTVALCN-RISATFAADTPTSCCFSYISRQIPQNFIADYFETNSQCSK 59
                                                     1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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Ishizuka K., Igata-Yi R., Naruse K., Nakashima H., Ohuchi K.,
Katsuragi S., Kin Y., Ohmoto Y., Nomiyama H., Iio M., Miura R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
"Comprehensive cloning and sequencing reveals evolutionary
conservation among all groups of rhesus macaque chemokines.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF449266; AAN76070.1; - SEQUENCE 92 AA: 10119 MW; 021CAA371143D12A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; D63785; BAA09855.1; -.
HSSP; P13236; 1HUM.
 Best Local Similarity 54.3%; Pred. No. 2.8e-28;
Matches 50; Conservative 19; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAX-2002 (TrEMBLrel. 20, Last annotation update)
1D78 alpha beta precursor (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                   61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                         60 PGIIFLTKRNRHVCADPKETWVQEIITDLELN 91
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                                                                                                                                                                                                                                                                  92 AA.
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Interpro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMAR; PS00049; SY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
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                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).
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                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9544;
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5 VIVLSILMLVAAFCSPALSAPMGSDPFTACCFSYTARKLPRNFVVDYYETSSLCSQPAVV 64
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                                                                                                                                                                                                                                                                                    2 LAVLLCTMALCN-QFSASLAADTPTACCFSYTSRQIPQNFMADYFETSSQCSKPSVIFLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hughes S.M., Bumstead N.; "Mapping of the gene encoding the chicken homologue of the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                      Score 271.5; DB 4; Length 80;
Pred. No. 1.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%; Score 264; DB 13; Length 90; 51.1%; Pred. No. 1.5e-24;
                                                                                                                                           55.9%; Score & .... 1.6e-25; 59.5%; Pred. No. 1.6e-25; arive 17; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEBL; AFIGURATO, AAD48772.11 -- HSSP; P13236; 1HUM.
INDEXPRO; 1FR000827; CC chemkine_sml.
IntexPro; 1FR001891; Chemckine_ILB.
Ffam; PF00048; ILB; 1.
SMART; SMO0199; SCY; 1.
SEQUENCE 90.4A; 9986 WW; SOAF9679A2675ICB CRC64;
1 1 POTENTIAL.
<1 16 POTENTIAL.
17 >80 LD78 ALPHA BETA.
80 80 80 80 80 80 80 80 885 09EB15648E971 CRC64;
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Last annotation update)
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                                                                                                                                                                                                         47; Conservative
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us-09-920-137a-7.rspt

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Query Match
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SIGNAL
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                                  SEQUENCE FROM N.A.

Hofmann R., Williams A.L., Swenerton R.K., Li P.-L.,

Hofmann-Lehmann R., Chenine A.-L., McClure H.M., Ruprecht R.M.;

"Quantification of Simian Cytckine and Beta-Chemckine mRNAs using

Real-Time Reverse-Transcriptase Polymerase Chain Reaction: Variations
in Expression during Chronic Primate Lentivirus Infection.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hofmann-Lehmann R., Williams A.L., Swenerton R.K., Li P.-L., Rasmussen R.A., Cherine A.-L., McClure H.M., Ruprecht R.M.; "Quantisication of Simian Cytokine and Beta-Chemokine mRNAs using Real-Time Reverse-Transcriptase Polymerase Chain Reaction: Variations in Expression during Chronic Primate Lentivirus Infection.", Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 PTACCESYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQEYV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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0
                                                                                                                                                                                                                                     35 CFSYTARKLPRNFVVDYYETSSLCSOPAVVFOTKRSKOVCADPSESWVQ 83
                                                                                                                                                                                                                                                   1 CFSYTVRKLPRNFVVDYYETSSLCSQPAVVFQTKRGKQVCADPSETWVQ 49
                                                                                                                                                                                    51.9%; Score 252; DB 6; Length 49; 93.9%; Pred. No. 2.2e-23; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.2%; Score 249; DB 6; Length 56; 73.2%; Pred. No. 6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                              49 AA; 5663 MW; D205B56BF349A6CA CRC64;
                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein 1 alpha (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AA; 6442 MW; EB12A0E0D41D6F68 CRC64;
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Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last seqn
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                                                                                                                                                                                               Conservative
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  Cercopithecinae, Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae, Macaca.
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Hofmann-Lehmann R.
             NCBI_TaxID=9544;
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SEQUENCE
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SEQUENCE
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796,
                                                                                                                                                                                                                                                                                                                                                                                                 50.5%; Score 245.5; DB 13; Length 89; 50.0%; Pred. No. 2.6e-22; Live 20; Mismatches 22; Indels 3;
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Submitted (Apr-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF506970; AAM34212.1; -
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR001811; Chemckine_IE8.
Ffam; PF00048; IL8; I.
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PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 91 AA; 10159 MW; AEBZ53E8CD4ED7FD CRC64;
                                                                                                                                                                                                                                                                                               POTENTIAL.
CHEMOKINE K203.
6FA2EA7A4950CA75 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 22, Last annotation update)
Small inducible Syckine A5 RANTES.
Equus caballus (Horse).
                                                                    Sick C., Schneider K., Staehell P., Weining K.C.;
"Novel chicken CXC and CC chemokines.";
Cytokine 12:181-186(2000).
EMBL, Y18692; CAB70956.1;
HSSP; P13236; 1HUM.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
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SEQUENCE FROM N.A.
MEDLINE=20170941; PubMed=10704244;
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                                                                                                                                                                                                InterPro; IPR001811; Chemokine_ILB.

    SIGNAL
    1
    21

    CHAIN
    22
    89

    SEQUENCE
    89 AA;
    9896 MW;

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                                                                                                                                                                                                                        Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
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les 43; Conserv
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1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                        1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=21655115; PubMed=11797102;

MEDLINE=21655115; PubMed=11797102;

Midne S., Haynes A., O'Regan M., Bumstead N.;

"Identification, mapping, and phylogenetic analysis of three novel chicken CC chemokines.";

Immunogenetics 53:74-683(2001).

EMBL, AV037859; AAK6443.1.;

InterPro; IPR001821; CC_chemkine sml.

InterPro; IPR001811; Chemokine_IEB.
                                   Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae; Macac
                                                                                                                                                     Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A., "Comprehensive cloning and sequencing reveals evolutionary conservation among 11 groups of rhesus macaque chemokines.", Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF449268; AAN76072.1; -
SEQUENCE 91 AA: 10019 MW; BCBD69ED0573803B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.0%; Score 233.5; DB 13; Length 91; 51.6%; Pred. No. 7.8e-21; tive 14; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                      DB 6; Length 91;
                                                                                                                                                                                                                                                                                 49.5%; Score 240.5; DB 6; Length 945.7%; Pred. No. 1.1e-21; tive 23; Mismatches 26; Indels
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SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 91 AA; 10154 MW; 744Ā64BB229194EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                   42; Conservative
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1es 47; Conservative
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                Chemokine CCL5/RANTES.
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                        NCBI_TaxID=9544;
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Matches
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Q8HYS0
ID Q8HYS1
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PRT;

PRELIMINARY;

QSHYSO

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1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                         DB 6; Length 91;
                                                                                                                                                                                                                                                                                                                                     ch 46.4%; Score 225.5; DB 6; Length Similarity 44.6%; Pred. No. 7.4e-20; 41; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                 SEQUENCE FROM N.A.

Enomoto A., Kano R., Hasegawa A.;

Enomoto J., Kano R., Hasegawa A.;

"molecular cloning of canine RANTES gene.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AB098562; BACS3725.1; -.

SEQUENCE 91 AA; 10179 MW; 01D79538CB8148E7 CRC64;
             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                        RANTES protein.
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08207A
FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                    Sequence 28, Appl
                                                                                                                                          December 16, 2003, 15:37:55 ; Search time 167.41 Seconds (without alignments) 500.045 Million cell updates/sec
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1 MKLCVIVUSLLMLVAAFCSP......VCADPSESWVQEYVYDLELN 92
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1: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

2: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

4: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

4: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

5: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

6: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

7: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

8: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

10: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

10: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

11: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

12: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

13: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

14: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

15: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

16: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

17: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

18: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

19: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

10: \cgn2 6/ptodata/1/paa/USOG_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Score Match Length DB
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APPLICANT: The Upjohn Company
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Hoogewerf, Arlene J. and Ledbetter, Steven R. TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND
TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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Sequence 7, Appl
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Sequence 11, Appl
Sequence 9374, A
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Sequence 9427, P
Sequence 9427, P
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Sequence 63102,
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US-08-136-117-28
US-08-136-117-28
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US-08-136-117-28
US-08-136-117-28
US-08-136-139-20
US-08-927-939-20
US-08-927-939-20
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US-09-113-705-4
US-09-113-705-1
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us-09-920-137a-7.rapm

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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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CORRESPONDENCE ADDRESS:
ADDRESSEE: The Upjohn Company, Intellectual Property Law
STREET: 301 Henrietta
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 486; DB 1; Length 92; ilarity 100.0%; Pred. No. 5.1e-48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hoogewerf, Arlene J.
APPLICANT: Lebetter, Steven
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND
TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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NAME: Jameson, William G.
REGISTRATION NUMBER: 27,199
REFERENCE/DOCKET NUMBER: 4731.1 CP
TELEPHONE: 616/385-7561
TELEPAX: 616/385-6897
                ATTORNEY/AGENT INFORMATION:
NAME: JameGon, William G.
REGISTRATION NUMBER: 27,199
REFERENCE/DOCKET NUMBER: 4731.1 CP
TELECHONE: 616/385-7561
TELEPHONE: 616/385-6897
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GENERAL INFORMATION:
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TELEX:
TELEX:
1NFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                        28:
                                                                                                                                                        TELEX: 224401
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                               LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
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tes 92; Conserv
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CLASSIFICATION:
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Query Match 100.0%; Score 486; DB 1; Length 92; Best Local Similarity 100.0%; Pred. No. 5.1e-48; Matches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               Sequence 10, Application PC/TUS9717900
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION:
MUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: F8815BO for Windows Version 2.0
CURTENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/17900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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FILING DATE: 30-SEP-1996
ATTONNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFRENCE/DOCKET NUMBER: 00786/29
TELECHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 10, Application PC/TUS9804002; GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
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PCT-US97-17900-10
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PCT-US98-04002-10
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RESULT 6
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GENERAL INFORMATION:
APPLICANT: Hoggewerf, Arlene J.
APPLICANT: Ledbetter, Steven R.
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND
TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Upjohn Company, Intellectual Property Law
STREET: 301 Henrietta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 486; DB 1; Length 92; Best Local Similarity 100.0%; Pred. No. 5.1e-48; Matches 92; Conservative 0; Mismatches 0; Indels
APPLICANT: Herrmann, Steve
APPLICANT: Swanberg, Stephen
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
TITLE OF INVENTION: CHEMCKINE DOMAINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/04002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Sprunger, Suzame
REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: G15291
TELECOMONINICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO:
LENGTH: 92 aming acids
                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 92 amino TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                                                           USA
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US-08-136-117-28
                                                                                                                                                                                                                           COUNTRY:
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 486; DB 5; Length 92; Best Local Similarity 100.0%; Pred. No. 5.1e-48; Matches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Coleman, Roger
APPLICANT: Wilde, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PAVVFOTKRSKOVCADPSESWVOEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0027 US
                                                                                                4731.1 CP
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DGS
SOFTWARE: FastSED Version 1.5
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Lither, Barbara J.
REGISTRATION WUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-00
TELECOMMUNICATION INFORMATION:
TELEFOXE 415-85-055
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acids
                                          NAME: Janeson, William G.
REGISTRATION NUMBER: 27,199
REFRENCE/DOCKET NUMBER: 4731
TELECOMMUNICATION INFORMATION:
TELEFAX: 616/385-7561
TELEFAX: 616/385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-08-136-117-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
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LIBRARY: GenBank
CLONE: MIP-1b
                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.
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us-09-920-137a-7.rapm

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61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
    61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-927-939A-20
                                                                                                                         US-08-927-939-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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                                                                                                                       1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYBTSSLCSQ 60
                                                                                                                                              1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLCVIVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Coleman, Roger
APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
ITILE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,
TITLE OF INVENTION: ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
                                    100.0%; Score 486; DB 7; Length 92; 100.0%; Pred. No. 5.1e-48; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 486; DB 8; Length 92; Best Local Similarity 100.0%; Pred. No. 5.1e-48; Matches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                             61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                   61 PAVVFOTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/08/467,123
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0026 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,346
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                US-08-467-123-4; Sequence 4, Application US/08467123; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33,994
REFERENCE FOR STATE OF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 855-0555
TELEFAX: (415) 855-0572
                                      Query Match
Best Local Similarity 100.(
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
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CALIFORNIA
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US-08-390-740B-7
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1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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100.0%; Score 486; DB 13; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
APPLICANT: Crainger, David J.
APPLICANT: Tatalick, Lauren Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 1543.001US1
CURRENT APPLICATION NUMBER: US/08/927,939A
CURRENT FILING DATE: 1997-11-09
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 486; DB 13; Similarity 100.0%; Pred. No. 5.1e-48; 92; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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; Sequence 20, Application US/08927939A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 10, Application US/08940687; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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GENERAL INFORMATION:
APPLICANT: Hedric, Joseph A.
APPLICANT: Hadric, Joseph A.
APPLICANT: Hard, Luquan
APPLICANT: Jotnik, Albert
APPLICANT: Green, Jonathan R.
TITLE OF INVENTION: Mammalian Chemokines; Related Reagents
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE DNAK RESEARCH Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 486; DB 13; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0
APPLICANT: Luster, Andrew D.
APPLICANT: Garcia-Zepeda, Eduardo A.
APPLICANT: Sarafi, Mindy N.
ITILE OF INTENTION: MCP-4 AND MCP-5: NOVEL CHEMOKINES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SUFTWARE: FastsGO for Windows Version 2.0
SUFRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,128
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bickey-Brady, Kristina
REGISTRATION NUMBER: 39,109
FEGISTRATION NUMBER: 39,109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPERENCE/DOCKET NUMBER: 001
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                umknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 901 Califo
CITY: Palo Alto
STATE: California
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STRANDEDNESS: unl
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                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 02110
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 486; DB 14; Length 92; Best Local Similarity 100.0%; Pred. No. 5.1e-48; Matches 92; Conservative 0; Mismatches 0; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,092
FLING DATE: 13-FBB-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin 34,090
REGISTRICATION NUMBER: 34,090
REGISTRICATION NUMBER: 34,090
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (650)496-1200
INFORMATION FOR EGQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09081230
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul
TITLOANT: Sheppard, Paul
TITLOANT: SEQUENCES: 54
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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SUPPLARES FASTEED for Windows Version 2.0
SUPPLARES FASTEED ADTR: APPLICATION DATE: APPLICATION NUMBER: US/09/081,230
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ATTORNEY/AGENT INFORMATION:
NAME: Lingenfelter, Susan E
REGISTRATION NUMBER: 41,156
REFERENCE/DOCKET NUMBER: 97-23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ZymoGenetics
STREET: 1201 Eastlake Ave. E.
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206-442-6675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-023-092-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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61 PAVVFQTKRSKQVCADFSESWVQEYVYDLELN 92

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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                 0; Gaps
                                                                                                                                      Query Match 100.0%; Score 486; DB 14; Length 92; Best Local Similarity 100.0%; Pred. No. 5.1e-48; Matches 92; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 486; DB 15; Length 92; 100.0%; Pred. No. 5.1e-48; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09113705
GENERAL INFORMATION:
APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: STUART, SUSAN G
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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APPLICATION NUMBER: US/09/113,705
                                                                                                                                                                                                                                                                                                    61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                              61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0031 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144
FILING DATE: 13.APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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92 amino acids
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                                         single
                                                                           MOLECULE TYPE: protein US-09-081-230-3
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MEDIUM TYPE: Floppy of
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                   TYPE: amino acid STRANDEDNESS: sir
                                                            linear
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Best Local Similarity
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                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-113-705-4
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1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCESYTARKLPRNFVVDYYETSSLCSQ 60
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100.0%; Score 486; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Grainger, David J.
APPLICANT: Tatalick, Lauen Marie
APPLICANT: Tatalick, Lauen Marie
APPLICANT: Tatalick, Lauen Marie
APPLICANT: Kanaly, Suzaine T.
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REPRENCE: 295.021031
CURRENT APPLICATION NUMBER: US/09/150,813
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: US 08/927939
EARLIER APPLICATION NUMBER: US 08/927939
EARLIER FILING DATE: 1997-09-11
NUMBER OF SEC 10 NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                         APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Coleman, Roger
APPLICANT: Stuart, Susan G
TITLE OF INVENTION: New CHEMOKINE EXPRESSED IN EOSINOPHILS
FILE REFERENCE: PF-0031-1 DIV
CURRENT APPLICATION NUMBER: US/09/113,705A
CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 3.0
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                         ; Sequence 7, Application US/09113705A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-150-813-20
; Sequence 20, Application US/09150813
; GENERAL INFORMATION:
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hes 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: MIP-1b
US-09-113-705-7
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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US-09-113-705-7
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                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Search completed: December 16, 2003, 15:46:43 Job time : 168.41 secs

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Sequence 1657, Ap
Sequence 1057, Ap
Sequence 1057, Ap
Sequence 1057, Ap
Sequence 1057, Ap
Sequence 1657, Ap
Sequence 5, Appli
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Sequence 1058, Ap
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                                                                                                                            December 16, 2003, 15:38:25; Search time 13.5738 Seconds (without alignments) 366.280 Million cell updates/sec
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                                                                                                                                                                                                                                                                     1 MKLCVTVLSLLMLVAAFCSP......VCADPSESWVQEYVYDLELN 92
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1: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-622-134-10

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US-10-1052-134-10

US-10-1052-134-10

US-10-1052-134-10

US-10-1052-134-10

US-10-1053-1703-42

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US-10-398-457-13
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US-60-487-610-1677
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US-10-398-457-8
US-10-398-457-9
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                      Run on:
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Appliant App
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APPLICANT: CARGILL, Michele
APPLICANT: HIANG, Hongjin
TITLE OF INVENTION: GENETIC DOLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
SOFTWARE: FALSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1677, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, MICHEL
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 92
                                                                       277, App
279, App
281, App
2476, Ap
15, Appl
35, Appl
                                                                                                                                                                                                                    2330, Ap
4, Appli
11, Appl
2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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Sequence
Sequence
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US-10-398-457-10
US-10-398-457-3
US-10-398-457-3
US-10-474-794-277
US-10-474-794-277
US-10-474-794-279
US-60-487-610-2476
US-10-398-457-3
US-10-398-457-3
US-10-398-457-3
US-10-398-457-3
US-10-398-457-3
US-10-487-610-2399
US-10-487-610-2399
US-10-668-733-21
US-10-668-733-21
US-10-668-733-21
US-10-668-733-21
US-10-668-733-21
US-10-668-733-21
US-10-688-733-21
US-10-688-733-21
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     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
  ; OKGANISH: 110.110
US-60-487-610-1666
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US-60-487-610-1677
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Best Local S
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100.0%; Pred. No. 3.3e-50;
tive 0; Mismatches 0; Indels
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STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                    61 PAVVPQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                          61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOSE, PETER J.
GRIFFITHS-JOHNSON, DAVID A.
HSUAN, JOHN J.
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REPLICATION NUMBER: US/10/622,134
FILING DATE: 18-Jul-2003
CLASSIPICATION: 424
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PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 28
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GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
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US-10-332-038A-9
; Sequence 9, Application US/10332038A
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.un
The 69; Conservative
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                            92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo Sapiens
US-10-332-038A-9
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Best Local Similarity
Matches 92; Conserva
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LENGTH: 69
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERPERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INPECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FRACESC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESEPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT PILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOCTWARE: PARESEQ for Mindows Version 4.0
                                                                                                                                                                        1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                               61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                         61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PAVVPQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                // Sequence 1051, Application US/60485450
// GENERAL INFORMATION:
// APPLICANT: CARGILL, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1057, Application US/60485450 ; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-60-485-450-1051
  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1677
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US-60-485-450-1057
                                                            Query Match
Best Local Similarity
Thes 92; Conserva'
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US-60-485-450-1051
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LENGTH: 92
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Best Local S
TYPE: PRT
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                                                                                           1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                       1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gryphon Therapeutics, Inc.
APPLICANT: Gryphon Therapeutics, Inc.
APPLICANT: Offord, Robin
APPLICANT: Gaertner, Hubert
APPLICANT: Hartley, Oliver
TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
FILE REPERENCE: 03504.271
CURRENT APPLICATION NUMBER: US/10/332,038A
CURRENT FILING DATE: 2003-05-06
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.2%; Score 375; DB 6; Length 69; 100.0%; Pred. No. 3e-37; ative 0; Mismatches 0; Indels
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APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: MITHORS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 PWGSDPPTACCESYTARKLPRNFVUDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQE 84
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78.3%; Pred. No. 2.4e-35;
tive 0; Mismatches 0; Indels 20; Gaps
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                                                                                                 FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US/08/615,232A
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9318984
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: GB 9408602
FILING DATE: 29-APR-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/291,038
FILING DATE: 14.Apr-1999
APPLICATION NUMBER: «UNKNOWN»
                                                                                                                                                                                                                                                                                                            NAME: WILSON, MARY J.
REGIGTATION UNDBER: 32,955
REFERENCE/DOCKET NUMBER: 550-32
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1667, Application US/60487610; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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Best Local Similarity 78.34
Matches 72; Conservative
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; ORGANISM: Homo sapiens
US-60-487-610-1667
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APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
FILE REPERENCE: WO465
CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.0
APPLICANT: CARGILL, Michele

APPLICANT: CARGILL, Michele

APPLICANT: CHANG, Sheng-Yung

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels 20; Gaps 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLCVIVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%; Score 359; DB 7; Length 72; 78.3%; Pred. No. 2.4e-35; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 73.5%; Score 357; DB 6; Length 69; Best Local Similarity 95.7%; Pred. No. 4e-35; Matches 66; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PAV-----EYVYDLELN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Application PC/TUS0321703
GENERAL INFORMATION:
APPLICANT: Rupp, Rabio
APPLICANT: Wang, Jianrui
APPLICANT: Zhou, Ping
APPLICANT: Chou, Ping
APPLICANT: Mehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/10398457
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Escherichia Coli
US-10-398-457-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-60-485-450-1052
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PCT-US03-21703-42
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LENGTH: 72
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US-60-485-450-1058
Sequence 1058, Application US/60485450
Sequence 1058, Application US/60485450
GENERAL INFORMATION:
APPLICANT: CREAGLL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: RESPONSE TO INTERPERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: RESPONSE TO INTERPERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFRENCE: CLOO1470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT PEPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: RESELECT FOR Windows Version 4.0
1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQ 83
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GENURAL INFORMATION:
GENURAL INFORMATION:
APPLICANT: GTYPON Therapeutics, Inc.
APPLICANT: GTYPON Therapeutics, Inc.
APPLICANT: Hartley, Oliver
TILLE OF INVENTION: Chemckine Receptor Modulators, Production and Use FILE REFERENCE: 05504.271
CURRENT APPLICATION WMBER: US/10/332,038A
CURRENT PILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US 60/217,683
PRIOR APPLICATION NUMBER: US 60/217,683
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Indels
                                                                                                                                 61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Mismatches
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Matches 52; Conserva
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LENGIH: 70
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                                              APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods and Materials Relating to Novel Polypeptides and Polynucl
FILE REFERENT HYS-B2 PCT
CURRENT APPLICATION NUMBER: PCT/US03/21703
CURRENT FILING DATE: 2003-07-09
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APPLICANT: HOLD,
INTERPETANT: HOLD,
HORD,
HO
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FRIOR FILING DATE: 2002-09-18
FRIOR FILING DATE: 2002-09-18
FRIOR FILING DATE: 2002-07-12
FRIOR PELICATION NUMBER: 60/395,402
FRIOR FILING DATE: 2002-07-12
FRIOR PELICATION NUMBER: PCT/US02/22858
FRIOR FILING DATE: 2002-07-13
FRIOR FILING DATE: 2002-07-13
FRIOR FILING DATE: 2002-07-21
FRIOR PLICATION NUMBER: 10/296,115
FRIOR FILING DATE: 2001-07-21
FRIOR FILING DATE: 2002-11-18
FRIOR FILING DATE: 2002-11-18
FRIOR FILING DATE: 2002-11-18
FRIOR FILING DATE: 2002-11-19
FRIOR FILING DATE: 2002-11-13
FRIOR FILING DATE: 2002-11-13
FRIOR FILING DATE: 2002-11-13
FRIOR FILING DATE: 2002-10-12
FRIOR FILING DATE: 2002-10-11
FRIOR FILING DATE: 2002-11-10
FRIOR FILING DATE: 2002-12-10
FREMAINING FILING DATE: 2002-12-10
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56.5%; Pred. No. 7.8e-28;
tive 19; Mismatches 20;
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    Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-60-487-610-1678
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Best Local Similarity
Matches 52, Conserv
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PCT-US03-21703-42
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Sequence 3, Application PC/TUS0328745
GENERAL INFORMATION:
APPLICANT: CHEMOKINE THERAPEUTICS CORP.
TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
FILE REFERENCE: $9296.00003
CURRENT APPLICATION NUMBER: PCT/US03/28745
CURRENT FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 1640
SOFTWARE: Patentin version 3.2
                                                                           RESULT 14
US-10-398-457-31
Sequence 31, Application US/10398457
Sequence 31, Application US/10398457
GENERAL INPORMATION:
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
CURRENT APPLICATION NUMBER: US/10/398,457
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ 1D NOS: 37
SOUTHARE: Patentin version 3.0
SEQ 1D NO 31
T.ENGTH: 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFOTKRSKQVCADPSESWVQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | SLAADTPTACCFSYTSRQIPONFIADYFETSSQCSRPGVIFLTKRSRQVCADPSEEWVQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
FEATURE:
OTHER SPATISMS
PCT-US03-28745-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.2%; Score 278; DB 6; Length 70; Best Local Similarity 68.1%; Pred. No. 8.6e-26; Matches 47; Conservative 13; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 56.6%; Score 275; DB 1; Length 69; Best Local Similarity 68.7%; Pred. No. 1.9e-25; Matches 46; Conservative 13; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 16, 2003, 15:47:23 Job time: 14.5738 secs
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61 KYVSDLELS 69
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PCT-US03-28745-3
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LENGTH: 69
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December 16, 2003, 15:39:40; Search time 24.6339 Seconds (without alignments) 694.592 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 7, Appli Sequence 4, Appli Sequence 7, Appli Sequence 11, Appl Sequence 3, Appli Sequence 30, Appl Sequence 30, Appl App] Sequence 7, Appli Sequence 20, Appl Sequence 31, Appl Sequence 10, Appl Sequence 49, Appl Seguence 49, Appl Seguence 2, Appli Sequence 31, Sequence 11, Description US-08-927-939-20 US-09-834-95A-31 1 US-09-824-194A-31 1 US-09-920-1376-7 2 US-10-137-655-7 4 US-10-157-75-7 5 US-10-293-705-11 1 US-09-771-023-11 1 US-09-792-793A-30 US-10-1375-209A-30 US-09-195-457-10 US-08-927-939-49 US-09-151-450-2 SUMMARIES Query Match Length DB 1000.0 10

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9 US-09-834-795A 11 US-09-834-7954 12 US-10-26-270 12 US-10-23-081 12 US-10-233-082 12 US-10-233-082	14 US-10-141-965- 15 US-10-223-085- 15 US-10-223-086- 15 US-10-223-088- 15 US-10-223-090- 15 US-10-223-090- 15 US-10-223-090-	15 US-10-223-083-33 15 US-10-223-089-33 12 US-08-927-939-19 9 US-09-151-450-3 9 US-09-908-599-3	9 US-09-334-923A- 9 US-09-334-958A- 9 US-09-908-600-3 11 US-09-834-794A 11 US-09-920-137A	12 US-10-13/-8 12 US-10-165-2 12 US-10-165-2 14 US-10-116-2 14 US-10-158-3
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                          APPLICANT: Grainger, David J.
APPLICANT: Grainger, Lauen Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 295.022031
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT FILING DATE: 1997-09-11
NUMBER OF SEG ID NOS: 83
SOFTWARE: FRSEED for Windows Version 3.0
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                         ; Sequence 20, Application US/08927939; Publication No. US20010006640A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-08-927-939-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
US-08-927-939-20
                                                                                                                                                                                                                                                                                                            SEQ ID NO 20
LENGTH: 92
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us-09-920-137a-7.rapb

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RESULT 4
US-09-920-137A-7
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Sequence 31, Application US/09834794A

Sequence 31, Application US_0030026777A1

GENERAL INFORMATION:

APPLICANT: Lawrence, Papsidero

APPLICANT: Lawrence, Papsidero

APPLICANT: Lawrence, Preserci

TILE OF INVENTION: Described and Treatment of Breast Cancer

FILE REPERBNCE: 3380/11127-US/09/834,794A

CURRENT APPLICATION NUMBER: US/09/834,794A

CURRENT APPLICATION NUMBER: 00/146,580

PRIOR APPLICATION NUMBER: 60/071,899

PRIOR FILING DATE: 1998-09-03

PRIOR PILING DATE: 1998-01-20

PRIOR PLING DATE: 1998-01-20

PRIOR APPLICATION NUMBER: 60/092,155

NUMBER OF SEQ ID NOS: 35

SOFTWARE PATENTION PATE: 1998-07-09

SOFTWARE PATENTION PATE: 1998-07-09

SOFTWARE PATENTION PATE: 1998-07-09
                APPLICANT: LOTO, Dyster APPLICANT: Lord, Preserving APPLICANT: Lord, Pyster APPLICANT: John, Pyster TILE OF INVENTION: Detection and Treatment of Breast Cancer FILE REFERENCE: 3300/11127-US3
CURRENT APPLICATION NUMBER: US/09/834,795A
CURRENT FILING DATE: 2001-04-12,
PRIOR PILING DATE: 1998-09-03
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
NUMBER OF SEO ID NOS: 35
SOFTWARE: Patentin version 3.0
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100.0%; Score 486; DB 11; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: Lawrence, Papsidero
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LENGIH: 92
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Sequence 7, Application US/09920137A
Publication No. U520030049725A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Bandman, Olga
APPLICANT: Wilde, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/10137655
Publication No. US20030138917A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Bandman, Olga
APPLICANT: BANDMAN, Olga
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                             E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0027 US
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ Version 1.5
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/920,137A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-00
TELECOMMUNICATION INFORMATION:
TELEFONE: 415-85-055
TELEFAX: 415-85-0195
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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MIP-1b
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                                                                                                                                                                                                                                                                                                      94304
                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                             STATE: CA
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us-09-920-137a-7.rapb

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US-10-057-275-7
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Wilde, Craig C.
Seilhamer, Jeffrey J.
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITS PRODUCTION AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASEBO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,366
FILING DATE: 29-May-2002
CLASSIFICATION OATA:
APPLICATION NUMBER: US/08/467,123B
FILING DATE: 0-JUN-1995
APPLICATION NUMBER: US 08/375,346
FILING DATE: 19-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                           NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/137,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/10158366
; Publication No. US20020142398A1
; GENERAL INFORMATION:
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: GenBactonE: MIP-1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-137-655-7
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilde, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 486; DB 14; Length 92; Best Local Similarity 100.0%; Pred. No. 6.2e-48; Matches 92; Conservative 0; Mismatches 0; Indele (
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV
TELECOMMUNICATION INFORMATION:
TELEPRONE: 415-555-0555
TELEFAX: 415-445-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TBM COMPATIBLE
SOFFWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/057,275
FILMG DATE: 25-381-2002
PRIOR APPLICATION NUMBER: US/08/390,740A
FILMG DATE: February 17, 1995
ATTONEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                 ;
TOPOLOGY: linear
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MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-158-366-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7, Application US/10057275; Publication No. US20020155545A1; GENERAL INFORMATION:
                                                                                                                                                                                                                               LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 92 amino acids
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Coleman, Roger
Bandman, Olga
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us-09-920-137a-7.rapb

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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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WESULE |
WESULE |
WESULE |
Sequence | 11, Application US/10293705 |
Publication Wo. US203008346841 |
GENERAL INFORMATION:
APPLICANT: Wilde Craig G. |
APPLICANT: Bandman, Olga |
APPLICANT: Bandman, Olga |
TITLE OF INVENTION: DNA ENCODING LIVER EXPRESSED CHEMOKINE FILE OF INVENTION: DNA ENCODING LIVER EXPRESSED CHEMOKINE FILE OF INVENTION: DNA ENCODING LIVER EXPRESSED CHEMOKINE FILE OF INVENTION UNMERR: US/10/293,705 |
CURRENT APPLICATION NUMBER: 09/208,83 |
PRIOR PILING DATE: 1998-12-09 |
PRIOR APPLICATION NUMBER: 09/798,143 |
PRIOR APPLICATION NUMBER: 09/398,143 |
PRIOR APPLICATION NUMBER: 09/398,143 |
PRIOR PILING DATE: 1999-02-10 |
NUMBER OF SEQ ID NOS: 12 |
SOFTWARE: PERL FROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 486; DB 15; Length 92; Best Local Similarity 100.0%; Pred. No. 6.2e-48; Matches 92; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20030083468A1 g127080
US-10-293-705-11
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US-09-771-023-11
| Sequence 11, Application US/09771023
| Sequence 11, Application US/09771023
| Sequence 11, Application US/09771023
| APPLICANT: Hardiman Gerard T. APPLICANT: Bacon, Kevin B. APPLICANT: Bacon, Kevin B. APPLICANT: Schall, Thomas J. APPLICANT: Schall, Thomas J. APPLICANT: Zlotnik, Albert TITE OF INVENTION: MAMMALIAN CX3C CHEMOKINE GENES
                                                                                                                                                                                                                                                                                                                                                                    61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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LIBRARY: GenBank
CLONE: MIP-1b
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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ORGANISM: Homo sapiens
                                                                                    US-10-057-275-7
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1 MKLCVSALSILLIVAAFCAPGFSAPMGSDPPTSCCFSYTARKIPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%; Score 461; DB 11; Length 92; 92.4%; Pred. No. 4.4e-45; ative 4; Mismatches 3; Indels
                                                                                                                CUNIMITY: 0.20
CUNIMITY: 0.20
CUNIMITY: 0.20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERAITING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/09/771,023
FILING DATE: 2001-01-25
CLASSIPICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/786,068
FILING DATE: 1997-01-21
FRIUM DATA: APPLICATION DATA:
APPLICATION NUMBER: US 08/590,828
FILING DATE: 24-JAN-1996
ATTORNEY/ABRITY INFRMATION:
NAME: CANING EMAIN P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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ADDRESSE: DNAX Research Institute
STRET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DX0569K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415-496-1200
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-771-023-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 92
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25 PMGSDPPTACCESYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKOVCADPSESWVQE 84
                                               24 APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQ 83
                                                                          1 APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.3%; Score 371; DB 9; Length 68; 100.0%; Pred. No. 5.8e-35; Live 0; Mismatches 0; Indels
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  0; Indels
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APPLICANT: Tatalick, Lauen Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 295.022U31
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FRSESQ for Windows Version 3.0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT PILLOR DATE: 1990-11.18
PRIOR APPLICATION NUMBER: US/09/195,457
PRIOR APPLICATION NUMBER: 08/470,323
PRIOR PLING DATE: 1995-06-06
PRIOR PLING DATE: 1995-06-14
PRIOR APPLICATION NUMBER: PCT/GB94/02006
PRIOR PLING DATE: 1993-09-14
PRIOR APPLICATION NUMBER: GB 9318984.3
PRIOR PILLING DATE: 1993-09-14
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
FILE REFERENCE: 550-33
                                                                                                                                                                                                                                                                                                                        // Sequence 10, Application US/09195457
// Patent No. US20020081623A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 49, Application US/08927939; Publication No. US20010006640A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 100.0
68; Conservative
69; Conservative
                                                                                                                                                 84 EYVYDLELN 92
                                                                                                                                                                                              61 EYVYDLELN 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YVYDLELN 68
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US-09-195-457-10
                                                                                                                                                                                                                                                                      RESULT 13
US-09-195-457-10
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LENGTH: 68
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Best Local Si
Matches 68;
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LENGTH: 93
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Matches
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APPLICANT: McDonald, John R.
APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: METHODS AND COMPOSITIONS AND DISORDERS
FILE REFERENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375,209A
CURRENT FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                         1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APMGSDPPTACCFSYTARKLPRNFVVDXYETSSLCSQPAVVFQTKRSKQVCADPSESWVQ 60
                                                                       0; Gaps
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             81.1%; Score 394; DB 14; Length 92; 77.2%; Pred. No. 1.9e-37; tive 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.2%; Score 375; DB 10; Length 69; Best Local Similarity 100.0%; Pred. No. 2.1e-35; Matches 69; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.2%; Score 375; DB 12; Length 69; 100.0%; Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Human Chemokine Polypeptide: MIP-1-Beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Human Chemokine Polypeptide: MIP-1-Beta US-10-375-209A-30
                                                                                                                                                                                                                 61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                              61 PAVVFLTKKGRQICADPSEPWVNEYVNDLELN 92
                                                                                                                                                                                                                                                                                                                                                             US-09-792-793A-30
; Sequence 30, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/10375209A Publication No. US20030215421A1 GENERAL INFORMATION: APPLICANT: MCDONAIG, John R. APPLICANT: Coggins, Philip
                                                               71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 EYVYDLELN 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homo sapien
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: homo sapien
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Best Local Similarity
                                       Best Local Similarity
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US-10-375-209A-30
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LENGTH: 69
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LENGTH: 69
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Best Local Similarity 58.7%; Pred. No. 5.5e-29;
Matches 54; Conservative 20; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02140

MEDUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BROWN, SCOTT
REGISTRATION NUMBER: 32,724
REPERENCE/DOCKET NUMBER: GI 5215-PCT-US
TELEPHONE: (617) 665-824
TELEPHONE: (617) 665-821
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                61 PSVIFLTKRGRQVCADPSEEWVQKYVSDLELS 92
                                                                                                                                              61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
TITLE OF INVENTION: STEM CELL INHIBITOR
MUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: GENETICS INSTITUTE, INC.
STREET: 87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: December 16, 2003, 15:48:24
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,116
                                                                                                                                                                                                                                             RESULT 15
US-09-151-450-2
; Sequence 2, Application US/09151450
; Patent No. US20010010935A1
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 93 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-151-450-2
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Best Local Similarity
Matches 54; Conserva
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December 16, 2003, 15:36:19; Search time 36.6995 Seconds (without alignments) 397.904 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 1107863 seqs, 158726573 residues
                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                   US-09-920-137A-7
                                                                                                                                                                Scoring table:
                                                                                                                              Perfect score:
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                                                                                                                                           Sequence:
                                                                                                                                                                                                  Searched:
                                                                     Run on:
                                                                                                                   Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Act-2 clone dene o	Act-2 gene product	Human MIP-1 alpha	MIP-1-beta Homo	Human chemokine MI	Human Act-2 protei	Human chemokine MI	HIV Nef1 fusion pr	HIV_Nef1 fusion pr
ID	AAR04220	AAR05900	AAR22712	AAR70798	AAW76225	AAW82717	AAB15789	AAM52445	AAM52446
DB	11	11	13	16	19	20	21	23	23
% Query Match Length DB ID	92	92	92	92	92	92	92	92	92
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	486	486	486	486	486	486	486	486	486
Result No.	-	7	е	4	Z,	w	7	ω	σ

oxia-regul Nefl fusi In GPCR re Ibeta. H	pAT 744 gene produ Human GPCR related HIV Nefl fusion pr pAT744 gene produc Angiotensin conver Human 1400 polypep Raf MTP1-bera nrof	d sequencine hard sequencine hard sequencine hard sequencine sequencin sequencine sequencine sequencine sequencine sequencine sequen	acid sequen beta chemok chemokine M MIP-lbeta p GPCR relata Synthetic e macrophage	Mouse lymphoxine m Human Stem Cell In LD78beta. Home sa Stem cell inhibito Varient stem cell MIP-1-alpha. Home Human MI10 protein Human chemokine Cl Human chemokine MI
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ALIGNMENTS

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Siebenlist U, Leonard WJ, Zipfel PJ, Irving SG, Kelly K;
                                                                                             Act-2 clone gene product is activated human periferal blood mononuclear cell (PBMC).
                                                                                                                         Periferal blood mononuclear cell; PBMC; lymphokine;
                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICE. (USDC ) US SEC OF COMMERCE.
                 AAR04220 standard; protein; 92 AA.
                                                                                                                                                                                                               88US-0312001.
                                                       (updated)
(updated)
(first entry)
                                                                                                                                                                                                                                88US-0312001
                                                                                                                                    cytokine; mitogen; ds.
                                                                                                                                                                                                                                                                                                  WPI; 1990-139708/18.
                                                                                                                                                                                                              16-DEC-1988;
                                                                                                                                                                                                                                16-DEC-1988;
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                        USN7312001-N.
                                                        25-MAR-2003
17-DEC-2001
                                                                          12-SEP-1990
                                                                                                                                                                                           13-MAR-1990.
                                    AAR04220;
RESULT 1
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system activation. The proteins may also be used to determine the presence of their receptors.
                                                                                                                                                             61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                              61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                   AAR22712 standard; Protein; 92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 1; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91WO-US06489
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                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-132088/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP.
                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                      Human MIP-1 alpha.
                                     92 AA;
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22-SEP-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1992.
                                                                                   92;
                                      Seguence
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                                                              Query Match
                                                                                     Matches
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                                                                                                                                                         (Note: Revised entry submitted to correct the patent number format of US Government cowned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/nnis_us.html.)
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                            1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSO 60
                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                           The lymphokine/cytokine-like proteins are associated with the inflammatory response and/or have mitogenic activities. Antigens assed to the proteins may be useful in detection and purification, especially in bioassays of various tumour cells or genetic defects in the inflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probes raised to the gene product may be used in bioassay of the product, useful in detecting tumour cells, genetic defects in the inflammatory response, or in vivo, for the detection of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIEBENLIST U, ZIPFEL PE, KELLEY K, IRVING SG, NAPOLITANO M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New lymphokine-cytokine-like genes - isolated by subtraction cloning and hybridisation using mRNA from activated peripheral blood T cells.
                                                                                                                                                                                                                                                        100.0%; Score 486; DB 11; Length 92; 100.0%; Pred. No. 4.4e-49; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Act-2; human lymphokine/cytokine-like protein; mitogenic; ds.
                      New lymphokine-cytokine genes -
isolated using mRNA from activated human periferal blood
mononuclear cells and T cells.
                                                                                                                                                                                                                                                                                                                                                           61 PAVVFOTKRSKOVCADPSESWVQEYVYDLELN 92
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                                                                      Disclosure, Page?; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89WO-US05603.
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                                                                                                                                                                                                                                                                                   92; Conservative
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                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Act-2 gene product.
                                                                                                                                                                                                                                    92 AA;
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N-PSDB; AAQ03682
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The protein was produced by cloning into the expression vector PYMIPSION. The human MIP-laipha sequence was derived from the lambda gt10 cDNA clone hMIP-lai, and the GAPDH promoter sequence, alpha factor transcription terminator derived from plasmid pdAll, the construction of which is described in patent application.

EP0324-274. Recombinantly produced MIP proteins have diagnostic and therapeutic utility for detecting and treating infections, cancer, welopoited evistuation and autoimmune diseases. Although not directly cytotoxic for WEH tumor calls, MPP-1 treated macrophages exhibited enhanced antibody-independent macrophage cytotoxicity for tumour targets. MPP-1 treatment stimulated proliferation of mature tissue macrophages; this effect was synergistic with both CSF-1 and CM-CSF. Purified preparations of the recombinantly derived CM-CSF. Purified preparations of the recombinantly derived MIP-lbeta did not. As little as twofold excess MIP-1beta blocked TNP-inducton by MIP-lalha a significant degree. Other
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                                                                                                  Gaps
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100.0%; Score 486; DB 11; Length 92; 100.0%; Pred. No. 4.4e-49; trive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macrophage inducible protein; cancer diagnosis; infection; myelopoietic dysfunction; autoimmune disease; ss.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purified heparanases, prepared under reducing conditions and activated with transglutaminase, are given in AAR70786-804. Most are prepared by reverse transcription of mRNA from activated human leukocytes, then cloning of the cDNA into pVL1392 baculovirus vector, and expression in Sf9 cells in the presence of reduced glutathione and dithiothreitol.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening for cpds. with anti-heparanase activity - by detecting inhibition of heparin or heparan sulphate degradation, potentially useful for treating arthritis, restenosis, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,
is the inhibition of proliferation of less differentiated erythropotetrin IL-3 dependent hematopoietic progenitor cells. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                             Macrophage inflammatory protein 1-beta; MIP-1-beta; heparanase; heparin; heparan sulfate; arthritis; restenosis;
                                                                    Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 486; DB 16; Length 92;
100.0%; Pred, No. 4.4e-49;
tive 0; Mismatches 0; Indels
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                Score 486; DB 13;
Pred. No. 4.4e-49;
0; Mismatches 0;
                                                                                                                                          61 PAVVFOTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                            61 PAVVEQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                           AAR70798 standard; Protein; 92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 47; 60pp; English.
                                                                100.0%;
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93US-0136117.
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                                                          Query Match
Best Local Similarity 100.0
Warches 92; Conservative
                                                                                                                                                                                                                                                 (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                  cancer; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-082239/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         (UPJO ) UPJOHN CO.
                                               92 AA;
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                                                                                                                                                                                                                                                                                                                                                     WO9504158-A1.
                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1993;
13-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                          09-FEB-1995.
                                                                                                                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                         29-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
                                                                                                                                                                                                                                                                            MIP-1-beta
                                                                                                                                                                                                                             AAR70798;
                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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This sequence represents a human chemokine MIP-lbeta domain, derived from HUMACT2A. This sequence is used in the production of a construct comprising an isolated polymuclectide encoding a chimeric polypeptide comprises at least 1 chemokine polypeptide covalently attached to at least 1 heterologous polypeptide. By including a heterologous protein construction, the chimeric polypeptides will have longer and increased biological activity and can direct the chemokine to a particular site. The chimeric polypeptides can also be designed to inhibit or desensitise chemokine receptors. They can be used to affect the chemotactic recruitment of migratory cells, e.g. for stimulating or inhibiting angiogenesis, for regeneration of bone, cartilage, ligament or for treating or preventing inflammatory or autoimmune disorders. They can contract and for preventing inflammatory or autoimmune disorders. They can be used as vaccine adjuvants or to enhance the activity of antigen or presenting cells and for treating or treventing HIV infection.

Set and the repentics for both conditions associated with the chemokine corresponding to the chimeric polypeptide and continue the absorbance of also the chemokine domain of the chimeric polypeptide and continue the chemokine corresponding to the chimeric polypeptide and continue the chemokine corresponding to the chimeric polypeptide and continue the chemokine corresponding to the chimeric polypeptide and corresponding to the chimeric polypeptide and corresponding to the chemokine corresponding to the chemokine domain of the chimeric polypeptide and corresponding to the chemokine corresponding t
Chemokine; MIP-lbeta; chimeric; human; heterologous protein; inhibitor; receptor; chemotaxis; migratory cell; angiogenesis; bone; regeneration; cartilage; ligament; tendon; bone marrow; transplant; inflammation; autofumune disorder; vaccine adjuvant; antigen presenting cell; cancer; HIV; human immunodeficiency virus; therapy; prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric polypeptide(s) - comprise chemokine polypeptide covalently linked to heterologous polypeptide, used for, e.g. chemotactic recruitment of migratory cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human chemokine MIP-1beta domain protein fragment.
                                                                                                                                                                                                                                                                                                                             61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                            61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 53; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW76225 standard; Protein; 92 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-495387/42.
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100.0%; Score 486; DB 19; Length 92; 100.0%; Pred. No. 4.4e-49;

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This sequence represents a human beta chemokine, Act-2 which is used to describe a method in which a novel beta chemokine, ZCHEMO-8 is isolated. Cascribe a method in which a novel beta chemokine, ZCHEMO-8 is isolated. Altered levels of ZCHEMO-8 indicative of pathological conditions, including infections, cancer, whelpopietic disorders, autoimmune closed and immunodeficiencies. The ZCHEMO-8 polypeptides can be used, sound healing regime to stimulate an infiltration of immune cells (e.g. wound healing regime to stimulate an infiltration of immune cells (e.g. monocytes, neutrophils, T lymphocytes or basophils to a wound site to the marrow into the peripheral blood for transplants. ZCHEMO-8 call trom the mediating suppression of HIV replication in CD4 T-cells and limiting progression of HIV infection to AIDS. Use may be made of ZCHEMO-8 polypeptides could be used to further define the role of chemokines in mediating suppression of HIV replication in CD4 T-cells and limiting progression of HIV infection to AIDS. Use may be made of ZCHEMO-8 progression of HIV infection to AIDS. Use may be made of ZCHEMO-8 certain macrophages, neutrophils, basophils, B lymphocytes and/or T cells may be effective. Such diseases where the inhibition of activation of certain macrophages, neutrophils, basophils, B lymphocytes and/or T cells may be effective. Such diseases include autoimmune diseases e.g. multiple sclerosis, insulin-dependent diabetes and systemic lupus erythematory and infective diseases. Antagonists may be used to dampen or inactivate and infective diseases. Antagonists may be used to dampen or inactivate zenemo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemokine; ZCHEMO-8; human; pathological condition; infection; cancer; autoimmune disorder; immunodeficiency; myelopoietic; wound healing; transplant; progenitor cell; HIV infection; AIDS; chemotherapy; radiation therapy; T cell; macrophage activation inhibitor; B lymphocyte; chronic inflammatory disease; infective disease; diagnosis; detection; drug screening; gene therapy; Act-2.
                                                                    1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                         1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human beta-chemokine, ZCHEMO-8 - used to develop products for treating e.g. ischaemia, reperfusion, wound healing, autoimmune diseases, inflammation, asthma or infections
  0; Indels
                                                                                                                                    61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                              61 PAVVFOTKRSKOVCADPSESWVQEYVYDLELN 92
0; Mismatches
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                                                                                                                                                                                                                                                                                              AAW82717 standard; Protein; 92 AA
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92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Act-2 protein.
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                              1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis; monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV; AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia; basophil-mediated disease; myocardial infarction; acute ischaemia; rheumatoid arthritis; contraception.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases, atherosolerosis, osteoporosis, HIV infection and AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated diseases, endoctoxaemia, myocardial infarction, acute ischaemia and rheumatoid arthritis, and can be used to prevent strokes and as contraceptives. The coding sequences for the chemokines can be used in gene therapy for the same diseases, as well as in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and for treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention concerns the identification of a number of chemokines which can be used to produce derivatives, agonists and antagonists which are then useful in disease treatment. The chemokines include sequences AAB15785-B15794, AAB15803-B15813 and AAB15813-B15813 These chemokine derivatives can be used to treat diseases such as
                                                                                                         Gaps
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0
                                                                        Length 92;
                                                                                                         Indels
for detection, diagnosis, drug screening or gene therapy
                                                                    100.0%; Score 486; DB 20;
100.0%; Pred. No. 4.4e-49;
live 0; Mismatches 0;
                                                                                                                                                                                                                61 PAVVFOTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                          61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human chemokine MIPlbeta SEQ ID NO: 20.
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                                                                                                                                                                                                                                                                                                                                          AAB15789 standard; Protein; 92 AA
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99US-0452406
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                                                                                                       92; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                    Sequence
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Matches

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The present invention relates to selenoproteins encoded in the genome of a virus, where the coding sequence of the selenoprotein is genetically engineered for expression in a nuclaic acid construct. The invention also discloses a method for identifying selenoprotein coding sequences, for detecting certain viruses (e.g. HIV or Boola), cancer and immune system disorders. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New selenoprotein for use in detecting certain viruses, e.g. human immunodeficiency virus (HIV) or Ebola, cancer and immune system
                                                                                                                                                Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Columns 73-76; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Nadimpalli RG, Ramanathan CS;
                                                                                                                                                                                                                                                                                                                                                                                         (UYGE-) UNIV GEORGIA RES FOUND INC.
AAM52446 standard; Protein; 92 AA.
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                                                                                                            HIV Nefl fusion protein #13
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                                                                       03-JUL-2002 (first entry)
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                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor EW,
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                                                                               1 MKLCVTVLSILMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                        1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
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                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New selenoprotein for use in detecting certain viruses, e.g. human immunodeficiency virus (HIV) or Ebola, cancer and immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                         Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.
         100.0%; Score 486; DB 21; Length 92; 100.0%; Pred. No. 4.4e-49;
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                                                                                                                                                          61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor EW, Nadimpalli RG, Ramanathan CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Columns 73-76; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                      AAM52445 standard; Protein; 92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0679493.
                                                                                                                                                                                                                                                                                                                                                                                                   HIV_Nef1 fusion protein #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-001203P.
95US-003112P.
                                                                                                                                                                                                                                                                                                                                                                03-JUL-2002 (first entry)
                                               Conservative
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                             Similarity
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             Local S...
92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                            AAM52445;
           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                              1 MKLCVTVLSLIMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemokine, MIP-lbeta; chimeric, human, heterologous protein; inhibitor; receptor; chemotaxis; migratory cell; angiogenesis; bone; regeneration; cartilage; ligament; tendon; bone marrow; transplant; inflammation; autoimmune disorder; vaccine adjuvant; antigen presenting cell; cancer; HIV; human immunodeficiency virus; therapy; prevention.
                                                        0; Gaps
Match 100.0%; Score 486; DB 23; Length 92; Local Similarity 100.0%; Pred. No. 4.4e-49; es 92; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human chemokine MIP-1beta domain protein from clone MPB-X.
                                                                                                                                                                                      61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                     PAVVFOTKRSKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                       AAW76223 standard; Protein; 331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
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RESULT 9

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Hypoxia-regulated protein #93.

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                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a human chemokine MIP-lbeta domain, isolated from cDNA clone MPB-X. This sequence is used in the production of a construct comprising an isolated polymuclectide encoding a chimeric comprises at least 1 chemokine polypeptide covalently attached to at least 1 heterologous polypeptide. By including a netached to at least 1 heterologous polypeptide. By including a heve construction, the chimeric polypeptides will have longer and increased biological activity and can direct the chemokine to a particular site. The chimeric polypeptides can also be chemokine to a particular site. The chimeric polypeptides can also be considered the chemotractic recruiting transplanted bone marrow constituting or inhibiting angiogenesis, for regeneration of bone, to affect the chemotractic recruitment of migratory cells, e.g. for stimulating or inhibiting angiogenesis, for regeneration of bone, confident to the chemotractic recruiting or prevention inflammatory or autoimmune disorders. They can also be used as vaccine adjuvants or to autoimmune disorders. They can also be used as vaccine adjuvants or to preventing HIV inflection. Neutralising antibodies binding to the chimeric polypeptide and also in the treatment of some forms of the chimeric polypeptide and also in the chemokine is involved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 486; DB 19; Length 331;
100.0%; Pred. No. 2.1e-48;
Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                         New chimeric polypeptide(s) - comprise chemokine polypeptide covalently linked to heterologous polypeptide, used for, e.g. chemotactic recruitment of migratory cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                      /note= "Chemokine domain"
                                     /label= signal
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                             Claim 16c; Page 50-51; 69pp; English.
            Location/Qualifiers
                                                             25.331
/label= MIP-1beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP65219 standard; Protein; 92 AA.
                                                                                                                                                                  98WO-US04002
                                                                                                                                                                                           97US-0808720
                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                             Swanberg SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                   WPI; 1998-495387/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 AA;
                                                                                                                                                                                                                                                                                   N-PSDB; AAV56825
                                                                                                                                                                                                                                            Herrmann SH,
                                                                                                                                                                                           28-FEB-1997;
                                                                                                               W09838212-A2
                                                                                                                                                                  27-FEB-1998;
                                                                                                                                         03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP65219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                        Peptide
                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
ABP65219
ID ABP65
XX
AC ABP65
XX
DT 12-NO
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The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/protecome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type inder two experimental conditions, and identifying agene that is differentially regulated in the two specialised cell types under experimental conditions. ABV7813. ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia regulated conditions, and for regulating tumourigenesis, anglogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatral stress, preeclapmist, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropolesis or hair loss.
Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigeneeis; anglogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclapmsia; atherosclerosis; inflammatory condition; wound healing; inflammation; erythropoiesis; hair loss; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPFTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLCVIVLSLIMLVAARCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a gene involved in disease for treating hypoxia-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conditions, comprises comparing the transcriptome/proteome of two types under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 483; DB 23; 98.9%; Pred. No. 9.9e-49; iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PAVVFQTKRSKQVCADPSETWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 35; Page 401; 538pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM52447 standard; Protein; 92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-2000; 2000GB-0030076.
08-FEB-2001; 2001GB-0003156.
25-OCT-2001; 2001GB-0025666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0-DEC-2001; 2001WO-GB05458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-627238/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulated gene
                                                                                                                                                                                                                                                                                                                                                             WO200246465-A2.
                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rayner WN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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27-SEP-2001; 2001US-325378P.
                                                                                                                                                                30-MAR-2001;
02-APR-2001;
02-MAY-2001;
                                                                                                                                                                                          02-MAY-2001;
02-MAY-2001;
17-MAY-2001;
                                                                                                                      22-MAR-2001;
23-MAR-2001;
                                                                                                                                               27-MAR-2001;
27-MAR-2001;
                                                                                                                                                                                                                   07-JUN-2001;
                                                                                                                                                                                                                           08-JUN-2001;
                                                                                                                                                                                                                                                                                       17-AUG-2001;
20-AUG-2001;
                                                                                                                                                                                                                                                                               16-AUG-2001;
                                                                                                                                                                                                                                                                      14-AUG-2001;
                                                                                                                                                                                                                                                                                                                          10-SEP-2001;
ò
                                                                                                                                                                                                                                                                 The present invention relates to selenoproteins encoded in the genome of a virus, where the coding sequence of the selenoprotein is genetically engineered for expression in a nucleic acid construct. The invention also discloses a method for identifying selenoprotein coding sequences, for detecting certain viruses (e.g. HIV or Ebola), cancer and immune system disorders. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                             1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDXYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                New selenoprotein for use in detecting certain viruses, e.g. human immunodeficiency virus (HIV) or Ebola, cancer and immune system
                                                Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.
                                                                                                                                                                                                                                                                                                                                              Query Match 99.2%; Score 482; DB 23; Length 92; Best Local Similarity 98.9%; Pred. No. 1.3e-48; Matches 91; Conservative 0; Mismatches 1; Indele
                                                                                                                                                                               Nadimpalli RG, Ramanathan CS;
                                                                                                                                                                                                                                                  Disclosure; Columns 73-76; 140pp; English.
                                                                                                                                                             (UYGE-) UNIV GEORGIA RES FOUND INC
                                HIV Nefl fusion protein #14.
                                                                                                                     96US-0679493.
                                                                                                                                     95US-001203P
                                                                                                                                             95US-003112P
              03-JUL-2002 (first entry)
                                                                                                                                                                                               WPI; 2002-024734/03.
                                                                                                                                                                                                                                                                                                                             92 AA;
                                                                                                                    12-JUL-1996;
                                                                                                                                   14-JUL-1995;
                                                                  Homo sapiens
                                                                                  US6303295-B1
                                                                                                                                             01-SEP-1995;
                                                                                                    16-OCT-2001
                                                                                                                                                                              Taylor EW,
                                                                                                                                                                                                                                  disorders -
AAM52447;
                                                                                                                                                                                                                                                                                                                              Sequence
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2001US-288066P. 2001US-288228P. 2001US-291766P.

2001US-296693P. 2001US-296856P. 2001US-303230P.

2001US-3132379 2001US-3109139 2001US-3121919 2001US-31219169 2001US-3131829 2001US-313629 2001US-313629 2001US-313629 2001US-313629 2001US-313629 2001US-313629

2001US-276776P 2001US-276739P 2001US-277239P 2001US-277338P 2001US-277338P 2001US-277338P 2001US-277833P 2001US-278152P 2001US-278152P 2001US-278152P 2001US-278152P

2001US-275601P.

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Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M, Burgess CE; Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL, Guo X; Shenoy SG, Padigaru W, Taupier RJ, Miller CE, Casman SJ, Pena CEA; Gangolli EA, Gusev V, Smithson G, Zerhusen BD, Gerlach V; Pochart PP, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK; Larochelle WJ, Zhong M, Khramtsov NV, Voss EZ, Herrmann JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOVX polypeptides and polynucleotides, useful for treating a syndrome related to a human disease associated with the NOVX polypeptide e.g.,
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-058423/05.
N-PSDB; ABX70479.
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1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60

Claim 1; Page 202; 413pp; English.

Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytostatic

08-MAR-2002; 2002WO-US07355.

WO200279398-A2

10-OCT-2002

Human GPCR related protein NOV36b.

03-MAR-2003 (first entry)

ABU52388;

ABU52388 standard; Protein; 92 AA

RESULT 13

The present invention relates to the isolation of novel human polypeptides referred to as NOVX (NOVI-NOV44), variants of these proteins, and the polynucleotide encoding them. The NOVX proteins of the invention are G-protein coupled receptor (GPCR) related proteins. The sequences of the invention are useful in the manufacture of a medicament for treating a syndrome related to a human disease associated with the polypeptides e.g. cancer. ABU52111-ABU52408 represent the human NOVX proteins of the invention.

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61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                   ABP62996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                               RESULT 15
                                                                                        ABP62996
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                                                                                                                                                     1 MKLCVIVLSLLVLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A claimed method for reducing the no. of circulating platelets in the bloodstream of a mammal comprises admin. of MIP-1 and/or MIP-2 or their analogues to induce such a reduction. The MIP-1, MIP-2 or analogue may be operatively linked to a carrier. The MIPs can be used to inhibit megakaryocytopoiesis to effect in vivo reduction of platelet nos. They can be used to treat disorders with excessively high platelet counts such as thrombocytosis, stroke, pulmonary emboliand myeloproliferative disorders.
                                                                                                                        1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ
                                                                                      O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macrophage inflammatory protein; megakaryocytopoiesis; MIP-1; MIP-2; thrombocythemia; reactive thrombocytosis; stroke; emboli; platelet; myeloproliferative disorder.
                                      Score 478; DB 24; Length 92;
Pred. No. 3.8e-48;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.9%; Score 476; DB 14; Length 92; 98.9%; Pred. No. 6.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suppression of megakaryocytopoiesis - by administration of macrophage inflammatory protein-1 or -2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                              61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                     61 PAVVPOTKRGKOVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 17; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                             AAR36770 standard; protein; 92 AA.
                                        98.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-US09671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                 Conservative
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                                    uery Match
est Local Similarity
atches 90; Conserv
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92 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9309799-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gewirtz AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIP-1beta.
                                                                                                                                                                                                                                                                                                                                                                                                      AAR36770;
Sequence
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The invention relates to an isolated polynuclectide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a manahalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

(I), (II) and (III) are useful for diagnostic evaluation of disorders.

(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheiner's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies
                                                                                                                                                                                                                                                                                               Human; vulnerary; dermatological; neuroprotective; nootropic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 96.3%; Score 468; DB 23; Length 92; Similarity 96.7%; Pred. No. 5.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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u C, Drmanac RT,
                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 433.
ABP62996 standard; Protein; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-2001; 2001WO-US27093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi V, Zhou .
                                                                                                                                         14-OCT-2002 (first entry)
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